

Human Nucleic Acid Sequences from Ovarian Tumor Tissue

The invention relates to human nucleic acid sequences from ovarian tumor tissue, which code for gene products or parts thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main cancer causes of death in women is ovarian cancer, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which play a role as candidate genes in ovarian cancer, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which are expressed elevated in ovarian tumor tissue.

The invention also relates to nucleic acid sequences Seq. ID Nos. 27, 32, 42, 46, 67, 76, 78, 80, 85, 88, 90, 108, and 112, which are expressed elevated in breast tumor tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides according to the sequence protocols Seq. ID Nos. 124-257 and 274-307.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID Nos. 124-257 and 274-307 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The invention also relates to phage-display phages, which are directed against a polypeptide or a fragment and which are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273 according to the invention.

The polypeptides of sequences Seq. ID Nos. 124-257 and 274-305 according to the invention can also be used as tools for finding active ingredients against ovarian cancer, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-123 and 258-273 for expression of polypeptides, which can be used as tools for finding active ingredients against ovarian cancer.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 124-257 and 274-305 as pharmaceutical agents in the gene therapy for treatment of ovarian cancer or for the production of a pharmaceutical agent for treatment of ovarian cancer.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 124-257 and 274-305.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-123 and 258-273, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-123 and 258-273 for use as vehicles for gene transfer.

Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes).

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus).

Singleton = A contig that contains only one sequence.

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins.

N = selectively the nucleotide A, T, G or C.

X = selectively one of the 20 naturally occurring amino acids.

Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for tumor-related candidate genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the ovarian tumor tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2**Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 68 was found which occurs 6.08 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 68

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0195 | 0.0179 | 1.0896 | 0.9178 |
| Breast | 0.0141 | 0.0244 | 0.5758 | 1.7366 |
| Small intestine | 0.0184 | 0.0165 | 1.1122 | 0.8991 |
| Ovary | 0.0030 | 0.0182 | 0.1645 | 6.0803 |
| Endocrine tissue | 0.0136 | 0.0226 | 0.6038 | 1.6562 |
| Gastrointestinal | 0.0211 | 0.0185 | 1.1390 | 0.8780 |
| Brain | 0.0126 | 0.0082 | 1.5299 | 0.6536 |
| Hematopoietic | 0.0080 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0847 | 0.1300 | 7.6946 |
| Hepatic | 0.0095 | 0.0065 | 1.4706 | 0.6800 |
| Heart | 0.0233 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0062 | 0.0143 | 0.4355 | 2.2964 |
| Stomach-esophagus | 0.0000 | 0.0153 | 0.0000 | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0054 | 0.0068 | 0.7930 | 1.2610 |
| Pancreas | 0.0066 | 0.0055 | 1.1966 | 0.8357 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0153 | 0.0043 | 3.5827 | 0.2791 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0136 | 0.5611 | 1.7821 |
| Uterus-general | 0.0153 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0384 | | | |
| Prostate hyperplasia | 0.0149 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0147 | | | |
| Cervix | 0.0426 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0047 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0178 | Hematopoietic | 0.0057 |
| Lung | 0.0108 | Skin-muscle | 0.0259 |
| Suprarenal gland | 0.0254 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0040 |
| Placenta | 0.0121 | Nerves | 0.0479 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0083 |
| | | Uterus_n | |

[illegible]

The result is as follows:

Electronic Northern for SEQ. ID NO.: 86

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0117 | 0.0128 | 0.9153 | 1.0926 |
| Breast | 0.0090 | 0.0169 | 0.5293 | 1.8893 |
| Small intestine | 0.0092 | 0.0331 | 0.2781 | 3.5964 |
| Ovary | 0.0030 | 0.0234 | 0.1279 | 7.8175 |
| Endocrine tissue | 0.0204 | 0.0426 | 0.4795 | 2.0856 |
| Gastrointestinal | 0.0211 | 0.0185 | 1.1390 | 0.8780 |
| Brain | 0.0274 | 0.0195 | 1.4020 | 0.7133 |
| Hematopoietic | 0.0107 | 0.1136 | 0.0941 | 10.6267 |
| Skin | 0.0184 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0194 | 0.2451 | 4.0800 |
| Heart | 0.0307 | 0.0137 | 2.2358 | 0.4473 |
| Testicles | 0.0115 | 0.0819 | 0.1406 | 7.1142 |
| Lung | 0.0104 | 0.0286 | 0.3629 | 2.7557 |
| Stomach-esophagus | 0.0290 | 0.0153 | 1.8908 | 0.5289 |
| Muscle-skeleton | 0.0188 | 0.0300 | 0.6282 | 1.5918 |
| Kidney | 0.0163 | 0.0342 | 0.4758 | 2.1016 |
| Pancreas | 0.0132 | 0.0110 | 1.1966 | 0.8357 |
| Penis | 0.0150 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0174 | 0.0234 | 0.7445 | 1.3433 |
| Uterus-endometrium | 0.0270 | 0.5277 | 0.0512 | 19.5264 |
| Uterus-myometrium | 0.0229 | 0.0408 | 0.5611 | 1.7821 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0160 | | | |
| Prostate hyperplasia | 0.0297 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0353 | | | |
| White blood cells | 0.0095 | | | |
| Cervix | 0.0106 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0000 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0000 |
| Hematopoietic | Endocrine tissue 0.0245 |
| Skin | Fetal 0.0000 |
| Hepatic | Gastrointestinal 0.0000 |
| Heart-blood vessels | Hematopoietic 0.0000 |
| Lung | Skin-muscle 0.0097 |
| Suprarenal gland | Testicles 0.0000 |
| Kidney | Lung 0.0010 |
| Placenta | Nerves 0.0000 |
| Prostate | Prostate 0.0155 |
| Sensory organs | Sensory Organs 0.0000 |
| | Uterus_n |

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 114 was found which occurs 6.94 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 114

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0117 | 0.0026 | 4.5763 | 0.2185 |
| Small intestine | 0.0026 | 0.0075 | 0.3403 | 2.9389 |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0030 | 0.0208 | 0.1439 | 6.9489 |
| Gastrointestinal | 0.0085 | 0.0025 | 3.3962 | 0.2944 |
| Brain | 0.0057 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0083 | 0.0102 | 0.8129 | 1.2302 |
| Stomach-esophagus | 0.0193 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0136 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0033 | 0.0000 | undef | 0.0000 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0064 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0305 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0445 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0213 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0136 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.1418 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0047 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0244 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0154 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0137 |
| | | Uterus_n | 0.0000 |

In an analogous procedure, the following Northernblots were also found:

Electronic Northern for SEQ. ID NO.: 1

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0078 | 0.0077 | 1.0170 | 0.9833 |
| Breast | 0.0179 | 0.0075 | 2.3818 | 0.4198 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0120 | 0.0364 | 0.3289 | 3.0402 |
| Endocrine tissue | 0.0119 | 0.0100 | 1.1887 | 0.8413 |
| Gastrointestinal | 0.0134 | 0.0139 | 0.9664 | 1.0348 |
| Brain | 0.0059 | 0.0103 | 0.5760 | 1.7362 |
| Hematopoietic | 0.0080 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0129 | 0.7353 | 1.3600 |
| Heart | 0.0148 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0351 | 0.0000 | undef |
| Lung | 0.0052 | 0.0164 | 0.3175 | 3.1494 |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0120 | 0.0120 | 0.9994 | 1.0006 |
| Kidney | 0.0109 | 0.0068 | 1.5861 | 0.6305 |
| Pancreas | 0.0017 | 0.0110 | 0.1496 | 6.6857 |
| Penis | 0.0180 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0106 | 0.6142 | 1.6282 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-general | 0.0204 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0160 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0061 | | | |
| Cervix | 0.0000 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0136 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0000 |
| Hematopoietic | Endocrine tissue 0.0245 |
| Skin | Fetal 0.0070 |
| Hepatic | Gastrointestinal 0.0122 |
| Heart-blood vessels | Hematopoietic 0.0057 |
| Lung | Skin-muscle 0.0032 |
| Suprarenal gland | Testicles 0.0154 |
| Kidney | Lung 0.0164 |
| Placenta | Nerves 0.0141 |
| Prostate | Nerves 0.0205 |
| Sensory organs | Prostate 0.0000 |
| | Sensory Organs 0.0083 |
| | Uterus_n |

Electronic Northern for SEQ. ID NO.: 2

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0026 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0182 | 0.0000 | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0015 | 0.0010 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0032 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0117 | 0.4920 | 2.0326 |
| Lung | 0.0031 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0022 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|--------|-------------------------|--------|
| % frequency | | LIBRARIES | |
| % frequency | | % frequency | |
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0035 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0171 |
| Lung | 0.0000 | Skin-muscle | 0.0194 |
| Suprarenal gland | 0.0000 | Testicles | 0.0082 |
| Kidney | 0.0000 | Lung | 0.0020 |
| Placenta | 0.0000 | Nerves | 0.0137 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 3

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0117 | 0.0026 | 4.5763 | 0.2185 |
| Breast | 0.0064 | 0.0019 | 3.4026 | 0.2939 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0075 | 0.4528 | 2.2083 |
| Gastrointestinal | 0.0000 | 0.0093 | 0.0000 | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0085 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0193 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-general | 0.0051 | 0.1908 | 0.0267 | 37.4714 |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0178 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0064 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0071 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0062 | Lung | 0.0164 |
| Placenta | 0.0061 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 4

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|----------------|-----|
| Bladder | | | | |
| Breast | 0.0000 | 0.0026 | 0.0000 undef | |
| Small intestine | 0.0051 | 0.0000 | undef 0.0000 | |
| Ovary | 0.0000 | 0.0000 | undef undef | |
| Endocrine tissue | 0.0000 | 0.0572 | 0.0000 undef | |
| Gastrointestinal | 0.0034 | 0.0075 | 0.4528 2.2083 | |
| Brain | 0.0019 | 0.0093 | 0.2071 4.8289 | |
| Hematopoietic | 0.0022 | 0.0021 | 1.0799 0.9260 | |
| Skin | 0.0013 | 0.0379 | 0.0353 28.3379 | |
| Hepatic | 0.0000 | 0.0000 | undef undef | |
| Heart | 0.0000 | 0.0065 | 0.0000 undef | |
| Testicles | 0.0053 | 0.0000 | undef 0.0000 | |
| Lung | 0.0000 | 0.0000 | undef undef | |
| Stomach-esophagus | 0.0104 | 0.0041 | 2.5402 0.3937 | |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef | |
| Kidney | 0.0017 | 0.0000 | undef 0.0000 | |
| Pancreas | 0.0027 | 0.0000 | undef 0.0000 | |
| Penis | 0.0083 | 0.0000 | undef 0.0000 | |
| Prostate | 0.0030 | 0.0000 | undef 0.0000 | |
| Uterus-endometrium | 0.0022 | 0.0000 | undef 0.0000 | |
| Uterus-myometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-general | 0.0051 | 0.0000 | undef 0.0000 | |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0035 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0278 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0093 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0114 |
| Lung | 0.0142 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0036 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0062 | Nerves | 0.0060 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0208 |
| | 0.0251 | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 5

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T T/N | |
|----------------------|-----------------------|----------------------|------------------------|-------|
| Bladder | | | | |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0130 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS % frequency | | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|----------------------|--------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 6

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0128 | 0.3051 | 3.2777 |
| Breast | 0.0141 | 0.0075 | 1.8715 | 0.5343 |
| Small intestine | 0.0123 | 0.0165 | 0.7415 | 1.3487 |
| Ovary | 0.0120 | 0.0390 | 0.3070 | 3.2573 |
| Endocrine tissue | 0.0290 | 0.0376 | 0.7698 | 1.2990 |
| Gastrointestinal | 0.0211 | 0.0324 | 0.6508 | 1.5365 |
| Brain | 0.0126 | 0.0144 | 0.8742 | 1.1439 |
| Hematopoietic | 0.0174 | 0.0000 | undef | 0.0000 |
| Skin | 0.0184 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0194 | 0.2451 | 4.0800 |
| Heart | 0.0106 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0173 | 0.0000 | undef | 0.0000 |
| Lung | 0.0218 | 0.0204 | 1.0669 | 0.9373 |
| Stomach-esophagus | 0.0193 | 0.0153 | 1.2605 | 0.7933 |
| Muscle-skeleton | 0.0137 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0190 | 0.0205 | 0.9252 | 1.0808 |
| Pancreas | 0.0099 | 0.0110 | 0.8974 | 1.1143 |
| Penis | 0.0150 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0109 | 0.0106 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0152 | 0.0408 | 0.3741 | 2.6732 |
| Uterus-general | 0.0306 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0192 | | | |
| Prostate hyperplasia | 0.0208 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0217 | | | |
| Cervix | 0.0319 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------------|---|
| Development | Breast 0.0476 |
| Gastrointestinal 0.0557 | Ovary_n 0.3190 |
| Brain 0.0167 | Ovary_t 0.0101 |
| Hematopoietic 0.0063 | Endocrine tissue 0.0000 |
| Skin 0.0079 | Fetal 0.0151 |
| Hepatic 0.0000 | Gastrointestinal 0.0000 |
| Heart-blood vessels 0.0000 | Hematopoietic 0.0057 |
| Lung 0.0213 | Skin-muscle 0.0000 |
| Suprarenal gland 0.0181 | Testicles 0.0309 |
| Kidney 0.0254 | Lung 0.0082 |
| Placenta 0.0185 | Nerves 0.0010 |
| Prostate 0.0121 | Prostate 0.0000 |
| Sensory organs 0.0000 | Sensory Organs 0.0310 |
| | Uterus_n 0.0458 |
| | |

Electronic Northern for SEQ. ID NO.: 7

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|----------------|-----|
| Bladder | 0.0000 | 0.0077 | 0.0000 undef | |
| Breast | 0.0026 | 0.0113 | 0.2268 4.4083 | |
| Small intestine | 0.0031 | 0.0331 | 0.0927 10.7893 | |
| Ovary | 0.0000 | 0.0182 | 0.0000 undef | |
| Endocrine tissue | 0.0051 | 0.0050 | 1.0189 0.9815 | |
| Gastrointestinal | 0.0057 | 0.0139 | 0.4142 2.4145 | |
| Brain | 0.0030 | 0.0010 | 2.8798 0.3472 | |
| Hematopoietic | 0.0027 | 0.0000 | undef 0.0000 | |
| Skin | 0.0000 | 0.0000 | undef undef | |
| Hepatic | 0.0000 | 0.0065 | 0.0000 undef | |
| Heart | 0.0000 | 0.0000 | undef undef | |
| Testicles | 0.0062 | 0.0123 | 0.5080 1.9684 | |
| Lung | 0.0000 | 0.0000 | undef undef | |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef | |
| Muscle-skeleton | 0.0163 | 0.0205 | 0.7930 1.2610 | |
| Kidney | 0.0017 | 0.0055 | 0.2991 3.3428 | |
| Pancreas | 0.0030 | 0.0000 | undef 0.0000 | |
| Penis | 0.0000 | 0.0021 | 0.0000 undef | |
| Prostate | 0.0000 | 0.0000 | undef undef | |
| Uterus-endometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-myometrium | 0.0064 | | | |
| Uterus-general | 0.0030 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0106 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0052 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0072 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0120 |
| Placenta | 0.0000 | Nerves | 0.0205 |
| Prostate | 0.0000 | Prostate | 0.0077 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|-----|
| Bladder | 0.0000 | 0.0000 | undef | undef | |
| Breast | 0.0064 | 0.0038 | 1.7013 | 0.5878 | |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 | |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef | |
| Endocrine tissue | 0.0068 | 0.0125 | 0.5434 | 1.8403 | |
| Gastrointestinal | 0.0000 | 0.0046 | 0.0000 | undef | |
| Brain | 0.0037 | 0.0000 | undef | 0.0000 | |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 | |
| Skin | 0.0000 | 0.0000 | undef | undef | |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef | |
| Heart | 0.0042 | 0.0137 | 0.3084 | 3.2426 | |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 | |
| Lung | 0.0031 | 0.0000 | undef | 0.0000 | |
| Lung | 0.0000 | 0.0000 | undef | undef | |
| Stomach-esophagus | 0.0000 | 0.0060 | 0.0000 | undef | |
| Muscle-skeleton | 0.0054 | 0.0068 | 0.7930 | 1.2610 | |
| Kidney | 0.0050 | 0.0000 | undef | 0.0000 | |
| Pancreas | 0.0120 | 0.0000 | undef | 0.0000 | |
| Penis | 0.0022 | 0.0000 | undef | 0.0000 | |
| Prostate | 0.0000 | 0.0000 | undef | undef | |
| Uterus-endometrium | 0.0000 | 0.0068 | 0.0000 | undef | |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef | |
| Uterus-general | 0.0089 | | | | |
| Breast hyperplasia | 0.0000 | | | | |
| Prostate hyperplasia | 0.0118 | | | | |
| Seminal vesicle | 0.0026 | | | | |
| Sensory organs | 0.0000 | | | | |
| White blood cells | | | | | |
| Cervix | | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0111 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0130 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0020 |
| Placenta | 0.0061 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0333 |
| | | Uterus_n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0038 | 0.0019 | 2.0416 | 0.4898 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0208 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0201 | 0.1698 | 5.8889 |
| Gastrointestinal | 0.0057 | 0.0000 | undef | 0.0000 |
| Brain | 0.0081 | 0.0072 | 1.1314 | 0.8839 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0010 | 0.0020 | 0.5080 | 1.9684 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0051 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0043 | 1.5354 | 0.6513 |
| Uterus-endometrium | 0.0068 | 0.1583 | 0.0427 | 23.4317 |
| Uterus-myometrium | 0.0152 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0149 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0093 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0057 |
| Lung | 0.0036 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0309 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0100 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0077 |
| | | Uterus_n | 0.0250 |

| | NORMAL % frequency | TUMOR % frequency | Ratios | |
|----------------------|-----------------------|----------------------|--------|--------|
| | | | N/T | T/N |
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0013 | 0.0019 | 0.6805 | 1.4694 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0182 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0051 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0009 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0125 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 12

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0156 | 0.0026 | 6.1018 | 0.1639 |
| Breast | 0.0102 | 0.0038 | 2.7221 | 0.3674 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0208 | 0.0000 | undef |
| Endocrine tissue | 0.0170 | 0.0201 | 0.8491 | 1.1778 |
| Gastrointestinal | 0.0057 | 0.0000 | undef | 0.0000 |
| Brain | 0.0126 | 0.0072 | 1.7485 | 0.5719 |
| Hematopoietic | 0.0080 | 0.0000 | undef | 0.0000 |
| Skin | 0.0220 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0065 | 0.7353 | 1.3600 |
| Heart | 0.0053 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0173 | 0.0000 | undef | 0.0000 |
| Lung | 0.0093 | 0.0061 | 1.5241 | 0.6561 |
| Stomach-esophagus | 0.0000 | 0.0153 | 0.0000 | undef |
| Muscle-skeleton | 0.0137 | 0.0180 | 0.7615 | 1.3133 |
| Kidney | 0.0054 | 0.0479 | 0.1133 | 8.8268 |
| Pancreas | 0.0083 | 0.0055 | 1.4957 | 0.6686 |
| Penis | 0.0150 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0087 | 0.0021 | 4.0945 | 0.2442 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0381 | 0.0068 | 5.6113 | 0.1782 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0095 | | | |
| Cervix | 0.0000 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | | Ovary_n | 0.0000 |
| Brain | 0.0139 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0083 | Endocrine tissue | 0.0000 |
| Skin | 0.0063 | Fetal | 0.0082 |
| Hepatic | 0.0118 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0057 |
| Lung | 0.0107 | Skin-muscle | 0.0259 |
| Suprarenal gland | 0.0072 | Testicles | 0.0154 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0247 | Nerves | 0.0040 |
| Prostate | 0.0182 | Prostate | 0.0205 |
| Sensory organs | 0.0249 | Sensory Organs | 0.0000 |
| | 0.0000 | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 13

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T T/N | |
|----------------------|-----------------------|----------------------|------------------------|--------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0026 | 0.0019 | 1.3611 | 0.7347 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0020 | 0.5080 | 1.9684 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0055 | 0.0000 | undef |
| Pancreas | 0.0030 | 0.0000 | undef | 0.0000 |
| Penis | 0.0044 | 0.0021 | 2.0473 | 0.4885 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | 0.0000 | undef | undef |
| Prostate hyperplasia | 0.0235 | 0.0000 | undef | undef |
| Seminal vesicle | 0.0000 | 0.0000 | undef | undef |
| Sensory organs | 0.0000 | 0.0000 | undef | undef |
| White blood cells | 0.0000 | 0.0000 | undef | undef |
| Cervix | 0.0000 | 0.0000 | undef | undef |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0068 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0077 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0020 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 15

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0026 | 1.5254 | 0.6555 |
| Breast | 0.0051 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0025 | 1.3585 | 0.7361 |
| Gastrointestinal | 0.0019 | 0.0000 | undef | 0.0000 |
| Brain | 0.0015 | 0.0010 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0000 | undef | 0.0000 |
| Heart | 0.0032 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0021 | 0.0020 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0086 | 0.0120 | 0.7139 | 1.4008 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0087 | 0.0064 | 1.3648 | 0.7327 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0059 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0035 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0057 |
| Heart-blood vessels | 0.0072 | Hematopoietic | 0.0032 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0061 | Lung | 0.0010 |
| Placenta | 0.0000 | Nerves | 0.0137 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 16

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0117 | 0.0179 | 0.6538 | 1.5296 |
| Breast | 0.0307 | 0.0226 | 1.3611 | 0.7347 |
| Small intestine | 0.0215 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0338 | 0.2657 | 3.7640 |
| Endocrine tissue | 0.0034 | 0.0050 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0192 | 0.0185 | 1.0354 | 0.9658 |
| Brain | 0.0074 | 0.0133 | 0.5538 | 1.8057 |
| Hematopoietic | 0.0067 | 0.0000 | undef | 0.0000 |
| Skin | 0.0257 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0065 | 0.7353 | 1.3600 |
| Heart | 0.0148 | 0.0137 | 1.0794 | 0.9265 |
| Testicles | 0.0115 | 0.0000 | undef | 0.0000 |
| Lung | 0.0353 | 0.0164 | 2.1591 | 0.4631 |
| Stomach-esophagus | 0.0387 | 0.0077 | 5.0421 | 0.1983 |
| Muscle-skeleton | 0.0154 | 0.0120 | 1.2850 | 0.7782 |
| Kidney | 0.0163 | 0.0274 | 0.5948 | 1.6813 |
| Pancreas | 0.0198 | 0.0166 | 1.1966 | 0.8357 |
| Penis | 0.0090 | 0.0267 | 0.3369 | 2.9678 |
| Prostate | 0.0196 | 0.0064 | 3.0709 | 0.3256 |
| Uterus-endometrium | 0.0338 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0384 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0178 | | | |
| Sensory organs | 0.0353 | | | |
| White blood cells | 0.0182 | | | |
| Cervix | 0.0426 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0139 | Breast | 0.0136 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.1595 |
| Brain | 0.0063 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0041 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0249 | Hematopoietic | 0.0114 |
| Lung | 0.0181 | Skin-muscle | 0.0130 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0000 | Lung | 0.0164 |
| Placenta | 0.0061 | Nerves | 0.0110 |
| Prostate | 0.0499 | Prostate | 0.0274 |
| Sensory organs | 0.0126 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0458 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0031 | 0.0165 | 0.1854 | 5.3946 |
| Ovary | 0.0030 | 0.0234 | 0.1279 | 7.8175 |
| Endocrine tissue | 0.0000 | 0.0125 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0046 | 0.0000 | undef |
| Brain | 0.0044 | 0.0021 | 2.1599 | 0.4630 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0065 | 0.7353 | 1.3600 |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef |
| Lung | 0.0104 | 0.0041 | 2.5402 | 0.3937 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0083 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0060 | 0.0000 | undef | 0.0000 |
| Penis | 0.0022 | 0.0021 | 1.0236 | 0.9769 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0096 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0118 | | | |
| Seminal vesicle | 0.0017 | | | |
| Sensory organs | 0.0319 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0203 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0039 | Fetal | 0.0128 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0259 |
| Lung | 0.0036 | Skin-muscle | 0.0077 |
| Suprarenal gland | 0.0000 | Testicles | 0.0164 |
| Kidney | 0.0062 | Lung | 0.0100 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0333 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 19

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T T/N | |
|----------------------|-----------------------|----------------------|------------------------|--------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0000 | 0.0019 | 0.0000 | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0050 | 0.0000 | undef |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0020 | 0.0000 | undef |
| Lung | 0.0000 | 0.0077 | 0.0000 | undef |
| Stomach-esophagus | 0.0051 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0022 | 0.0000 | undef | 0.0000 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS % frequency | | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|----------------------|--------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0029 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0071 | Hematopoietic | 0.0065 |
| Lung | 0.0000 | Skin-muscle | 0.0077 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0020 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 20

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0019 | 0.6805 | 1.4694 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0208 | 0.0000 | undef |
| Endocrine tissue | 0.0051 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0030 | 0.0021 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0032 | 0.0137 | 0.2313 | 4.3235 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0073 | 0.0020 | 3.5562 | 0.2812 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0050 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0044 | 0.0021 | 2.0473 | 0.4885 |
| Prostate | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0032 | | | |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0061 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED LIBRARIES | |
|---------------------|-------------|--------------------------------------|-------------|
| | % frequency | | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0029 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0171 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0015 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0020 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0155 |
| Sensory organs | | Sensory Organs | 0.0000 |
| | | Uterus n | |

Electronic Northern for SEQ. ID NO.: 22

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0026 | 0.0000 | undef |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0165 | 0.0000 | undef |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0068 | 0.0000 | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0000 | 0.0051 | 0.0000 | undef |
| Breast | 0.0051 | 0.0019 | 2.7221 | 0.3674 |
| Small intestine | 0.0031 | 0.0331 | 0.0927 | 10.7893 |
| Ovary | 0.0000 | 0.0182 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0100 | 0.3396 | 2.9444 |
| Gastrointestinal | 0.0096 | 0.0093 | 1.0354 | 0.9658 |
| Brain | 0.0059 | 0.0021 | 2.8798 | 0.3472 |
| Hematopoietic | 0.0000 | 0.0379 | 0.0000 | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0129 | 0.0000 | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0042 | 0.0061 | 0.6774 | 1.4763 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0137 | 0.1983 | 5.0439 |
| Pancreas | 0.0099 | 0.0055 | 1.7949 | 0.5571 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0021 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0064 | 0.0000 | 0.0059 | 0.0000 |
| Prostate hyperplasia | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| Seminal vesicle | 0.0000 | 0.0017 | 0.0000 | 0.0000 |
| Sensory organs | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| White blood cells | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| Cervix | 0.0000 | 0.0000 | 0.0000 | 0.0000 |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T T/N | |
|----------------------|-----------------------|----------------------|------------------------|--------|
| Bladder | 0.0195 | 0.0077 | 2.5424 | 0.3933 |
| Breast | 0.0064 | 0.0075 | 0.8507 | 1.1756 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0153 | 0.0226 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0077 | 0.0093 | 0.8283 | 1.2072 |
| Brain | 0.0081 | 0.0092 | 0.8800 | 1.1364 |
| Hematopoietic | 0.0067 | 0.0379 | 0.1764 | 5.6676 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0194 | 0.2451 | 4.0800 |
| Heart | 0.0106 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0083 | 0.0102 | 0.8129 | 1.2302 |
| Stomach-esophagus | 0.0000 | 0.0153 | 0.0000 | undef |
| Muscle-skeleton | 0.0103 | 0.0180 | 0.5711 | 1.7510 |
| Kidney | 0.0081 | 0.0068 | 1.1896 | 0.8406 |
| Pancreas | 0.0033 | 0.0000 | undef | 0.0000 |
| Penis | 0.0329 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0153 | 0.0064 | 2.3885 | 0.4187 |
| Uterus-endometrium | 0.0135 | 0.1055 | 0.1280 | 7.8106 |
| Uterus-myometrium | 0.0305 | 0.0136 | 2.2445 | 0.4455 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0069 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0139 | Breast | 0.0136 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0203 |
| Hematopoietic | 0.0157 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0099 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0171 |
| Lung | 0.0000 | Skin-muscle | 0.0097 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0060 |
| Placenta | 0.0121 | Nerves | 0.0205 |
| Prostate | 0.0249 | Prostate | 0.0387 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0250 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 25

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0204 | 0.1907 | 5.2444 |
| Breast | 0.0141 | 0.0263 | 0.5347 | 1.8702 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0312 | 0.2878 | 3.4745 |
| Endocrine tissue | 0.0136 | 0.0150 | 0.9057 | 1.1042 |
| Gastrointestinal | 0.0192 | 0.0185 | 1.0354 | 0.9658 |
| Brain | 0.0222 | 0.0113 | 1.9635 | 0.5093 |
| Hematopoietic | 0.0094 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0129 | 0.3676 | 2.7200 |
| Heart | 0.0148 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0234 | 0.0000 | undef |
| Lung | 0.0135 | 0.0123 | 1.1007 | 0.9085 |
| Stomach-esophagus | 0.0097 | 0.0153 | 0.6303 | 1.5866 |
| Muscle-skeleton | 0.0188 | 0.0300 | 0.6282 | 1.5918 |
| Kidney | 0.0163 | 0.0205 | 0.7930 | 1.2610 |
| Pancreas | 0.0083 | 0.0221 | 0.3739 | 2.6743 |
| Penis | 0.0090 | 0.0267 | 0.3369 | 2.9678 |
| Prostate | 0.0109 | 0.0043 | 2.5591 | 0.3908 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0204 | 0.3741 | 2.6732 |
| Uterus-general | 0.0102 | 0.0954 | 0.1067 | 9.3678 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0087 | | | |
| Cervix | 0.0000 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0111 | Ovary_n | 0.1595 |
| Brain | 0.0000 | Ovary_t | 0.0203 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0058 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0488 |
| Heart-blood vessels | 0.0107 | Hematopoietic | 0.0114 |
| Lung | 0.0072 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0124 | Lung | 0.0164 |
| Placenta | 0.0000 | Nerves | 0.0060 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 26

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0234 | 0.0204 | 1.1441 | 0.8741 |
| Breast | 0.0192 | 0.0470 | 0.4083 | 2.4491 |
| Small intestine | 0.0184 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0546 | 0.1645 | 6.0803 |
| Endocrine tissue | 0.0204 | 0.0075 | 2.7170 | 0.3681 |
| Gastrointestinal | 0.0268 | 0.0416 | 0.6443 | 1.5522 |
| Brain | 0.0037 | 0.0154 | 0.2400 | 4.1669 |
| Hematopoietic | 0.0147 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0476 | 0.0259 | 1.8382 | 0.5440 |
| Heart | 0.0095 | 0.0412 | 0.2313 | 4.3235 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0166 | 0.0184 | 0.9032 | 1.1072 |
| Stomach-esophagus | 0.0387 | 0.0460 | 0.8404 | 1.1900 |
| Muscle-skeleton | 0.0069 | 0.0300 | 0.2284 | 4.3775 |
| Kidney | 0.0543 | 0.0411 | 1.3217 | 0.7566 |
| Pancreas | 0.0363 | 0.0110 | 3.2906 | 0.3039 |
| Penis | 0.0060 | 0.0267 | 0.2246 | 4.4517 |
| Prostate | 0.0218 | 0.0128 | 1.7060 | 0.5862 |
| Uterus-endometrium | 0.0338 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0136 | 0.0000 | undef |
| Uterus-general | 0.0051 | 0.0954 | 0.0534 | 18.7357 |
| Breast hyperplasia | 0.0352 | | | |
| Prostate hyperplasia | 0.0535 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0078 | | | |
| Cervix | 0.0106 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------------|---|
| Development | Breast 0.0204 |
| Gastrointestinal 0.0000 | Ovary_n 0.0000 |
| Brain 0.0083 | Ovary_t 0.0101 |
| Hematopoietic 0.0000 | Endocrine tissue 0.0000 |
| Skin 0.0039 | Fetal 0.0017 |
| Hepatic 0.0000 | Gastrointestinal 0.0244 |
| Heart-blood vessels 0.0000 | Hematopoietic 0.0000 |
| Lung 0.0000 | Skin-muscle 0.0000 |
| Suprarenal gland 0.0000 | Testicles 0.0000 |
| Kidney 0.0062 | Lung 0.0040 |
| Placenta 0.0121 | Nerves 0.0137 |
| Prostate 0.0249 | Prostate 0.0000 |
| Sensory organs 0.0000 | Sensory Organs 0.0083 |
| | Uterus_n |

Electronic Northern for SEQ. ID NO.: 27

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0000 | 0.0026 | 0.0000 | undef |
| Breast | 0.0013 | 0.0038 | 0.3403 | 2.9389 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0074 | 0.0051 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0027 | 0.0379 | 0.0706 | 14.1689 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0032 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0021 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0054 | 0.0068 | 0.7930 | 1.2610 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0090 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0128 | 0.1706 | 5.8615 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0089 | | | |
| Prostate hyperplasia | 0.0235 | | | |
| Seminal vesicle | 0.0017 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0041 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0114 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0124 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0030 |
| Prostate | 0.0000 | Prostate | 0.0137 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 28

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0026 | 0.0000 | undef |
| Breast | 0.0090 | 0.0038 | 2.3818 | 0.4198 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0119 | 0.0100 | 1.1887 | 0.8413 |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0015 | 0.0031 | 0.4800 | 2.0835 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0041 | 0.2540 | 3.9367 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0034 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0109 | 0.0043 | 2.5591 | 0.3908 |
| Uterus-endometrium | 0.0068 | 0.0528 | 0.1280 | 7.8106 |
| Uterus-myometrium | 0.0000 | 0.0136 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0059 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0213 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0076 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0217 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0124 | Lung | 0.0030 |
| Placenta | 0.0121 | Nerves | 0.0137 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 29

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0000 | 0.0019 | 0.0000 | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0010 | 0.0020 | 0.5080 | 1.9684 |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0021 | 0.0000 | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0051 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0009 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0032 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0020 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 30

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0078 | 0.0026 | 3.0509 | 0.3278 |
| Breast | 0.0038 | 0.0113 | 0.3403 | 2.9389 |
| Small intestine | 0.0123 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0702 | 0.0426 | 23.4526 |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0556 | 0.0278 | 2.0018 | 0.4995 |
| Brain | 0.0000 | 0.0010 | 0.0000 | undef |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0323 | 0.0000 | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0062 | 0.0082 | 0.7621 | 1.3122 |
| Lung | 0.0097 | 0.0077 | 1.2605 | 0.7933 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0110 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0065 | 0.0255 | 0.2559 | 3.9077 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0192 | | | |
| Uterus-general | 0.0357 | | | |
| Breast hyperplasia | 0.0890 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0213 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0167 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0017 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0137 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 31

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0026 | 1.5254 | 0.6555 |
| Breast | 0.0000 | 0.0019 | 0.0000 | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0046 | 0.0000 | undef |
| Brain | 0.0000 | 0.0010 | 0.0000 | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0032 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0021 | 0.0123 | 0.1693 | 5.9051 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Suprarenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0061 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |
| Breast | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0000 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles | 0.0000 |
| Lung | 0.0000 |
| Nerves | 0.0000 |
| Prostate | 0.0000 |
| Sensory Organs | |
| Uterus_n | |

Electronic Northern for SEQ. ID NO.: 32

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0038 | 0.0075 | 0.5104 | 1.9593 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0077 | 0.0000 | undef | 0.0000 |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0010 | 0.0000 | undef | 0.0000 |
| Lung | 0.0000 | 0.0153 | 0.0000 | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0022 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0118 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | | Sensory Organs | 0.0042 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 33

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0663 | 0.0741 | 0.8942 | 1.1183 |
| Breast | 0.0640 | 0.0846 | 0.7561 | 1.3225 |
| Small intestine | 0.1104 | 0.0165 | 6.6733 | 0.1499 |
| Ovary | 0.0958 | 0.1951 | 0.4912 | 2.0358 |
| Endocrine tissue | 0.0511 | 0.0426 | 1.1987 | 0.8343 |
| Gastrointestinal | 0.1188 | 0.1527 | 0.7781 | 1.2851 |
| Brain | 0.0584 | 0.0863 | 0.6771 | 1.4769 |
| Hematopoietic | 0.1016 | 0.1136 | 0.8940 | 1.1186 |
| Skin | 0.0698 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0776 | 0.0613 | 16.3199 |
| Heart | 0.1304 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0230 | 0.0819 | 0.2811 | 3.5571 |
| Lung | 0.1620 | 0.1227 | 1.3209 | 0.7571 |
| Stomach-esophagus | 0.0580 | 0.1073 | 0.5402 | 1.8511 |
| Muscle-skeleton | 0.1045 | 0.0480 | 2.1773 | 0.4593 |
| Kidney | 0.0516 | 0.0959 | 0.5381 | 1.8583 |
| Pancreas | 0.0529 | 0.1491 | 0.3545 | 2.8205 |
| Penis | 0.0749 | 0.0800 | 0.9360 | 1.0684 |
| Prostate | 0.0632 | 0.0426 | 1.4843 | 0.6737 |
| Uterus-endometrium | 0.0676 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.1067 | 0.2309 | 0.4621 | 2.1640 |
| Uterus-general | 0.1528 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0480 | | | |
| Prostate hyperplasia | 0.0476 | | | |
| Seminal vesicle | 0.0534 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.1309 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0333 | Ovary_t | 0.1595 |
| Hematopoietic | 0.0626 | Endocrine tissue | 0.0152 |
| Skin | 0.0590 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0052 |
| Heart-blood vessels | 0.0260 | Hematopoietic | 0.0244 |
| Lung | 0.0391 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0650 | Testicles | 0.0097 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0432 | Nerves | 0.0573 |
| Prostate | 0.0424 | Prostate | 0.0181 |
| Sensory organs | 0.0249 | Sensory Organs | 0.0342 |
| | 0.0126 | Uterus n | 0.0000 |
| | | | 0.0333 |

0022000231320

Electronic Northern for SEQ. ID NO.: 34

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|-----|
| Bladder | 0.0000 | 0.0000 | undef | undef | |
| Breast | 0.0038 | 0.0000 | undef | 0.0000 | |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 | |
| Ovary | 0.0030 | 0.0598 | 0.0501 | 19.9782 | |
| Endocrine tissue | 0.0068 | 0.0000 | undef | 0.0000 | |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef | |
| Brain | 0.0030 | 0.0000 | undef | 0.0000 | |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef | |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 | |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 | |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 | |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef | |
| Lung | 0.0042 | 0.0000 | undef | 0.0000 | |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef | |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef | |
| Kidney | 0.0299 | 0.0000 | undef | 0.0000 | |
| Pancreas | 0.0000 | 0.0000 | undef | undef | |
| Penis | 0.0000 | 0.0000 | undef | undef | |
| Prostate | 0.0000 | 0.0000 | undef | undef | |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef | |
| Uterus-myometrium | 0.0000 | | | | |
| Uterus-general | 0.0000 | | | | |
| Breast hyperplasia | 0.0000 | | | | |
| Prostate hyperplasia | 0.0000 | | | | |
| Seminal vesicle | 0.0000 | | | | |
| Sensory organs | 0.0106 | | | | |
| White blood cells | | | | | |
| Cervix | | | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast |
| Gastrointestinal | Ovary_n |
| Brain | Ovary_t |
| Hematopoietic | Endocrine tissue |
| Skin | Fetal |
| Hepatic | Gastrointestinal |
| Heart-blood vessels | Hematopoietic |
| Lung | Skin-muscle |
| Suprarenal gland | Testicles |
| Kidney | Lung |
| Placenta | Nerves |
| Prostate | Prostate |
| Sensory organs | Sensory Organs |
| | Uterus n |

Electronic Northern for SEQ. ID NO.: 35

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|-----|
| Bladder | 0.0000 | 0.0026 | 0.0000 undef | |
| Breast | 0.0000 | 0.0038 | 0.0000 undef | |
| Small intestine | 0.0061 | 0.0000 | undef 0.0000 | |
| Ovary | 0.0030 | 0.0234 | 0.1279 7.8175 | |
| Endocrine tissue | 0.0000 | 0.0000 | undef undef | |
| Gastrointestinal | 0.0192 | 0.0185 | 1.0354 0.9658 | |
| Brain | 0.0015 | 0.0062 | 0.2400 4.1669 | |
| Hematopoietic | 0.0013 | 0.0000 | undef 0.0000 | |
| Skin | 0.0000 | 0.0000 | undef undef | |
| Hepatic | 0.0000 | 0.0000 | undef undef | |
| Heart | 0.0000 | 0.0000 | undef undef | |
| Testicles | 0.0052 | 0.0061 | 0.8467 1.1810 | |
| Lung | 0.0000 | 0.0000 | undef undef | |
| Stomach-esophagus | 0.0000 | 0.0060 | 0.0000 undef | |
| Muscle-skeleton | 0.0027 | 0.0000 | undef 0.0000 | |
| Kidney | 0.0000 | 0.0110 | 0.0000 undef | |
| Pancreas | 0.0000 | 0.0000 | undef undef | |
| Penis | 0.0000 | 0.0000 | undef undef | |
| Prostate | 0.0000 | 0.0000 | undef undef | |
| Uterus-endometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0030 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0051 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 36

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|-----|
| Bladder | | | | |
| Breast | 0.0039 | 0.0000 | undef 0.0000 | |
| Small intestine | 0.0026 | 0.0000 | undef 0.0000 | |
| Ovary | 0.0000 | 0.0000 | undef undef | |
| Endocrine tissue | 0.0000 | 0.0130 | 0.0000 undef | |
| Gastrointestinal | 0.0000 | 0.0025 | 0.0000 undef | |
| Brain | 0.0000 | 0.0139 | 0.0000 undef | |
| Hematopoietic | 0.0022 | 0.0000 | undef 0.0000 | |
| Skin | 0.0027 | 0.0000 | undef 0.0000 | |
| Hepatic | 0.0073 | 0.0000 | undef 0.0000 | |
| Heart | 0.0000 | 0.0000 | undef undef | |
| Testicles | 0.0000 | 0.0137 | 0.0000 undef | |
| Lung | 0.0000 | 0.0234 | 0.0000 undef | |
| Stomach-esophagus | 0.0021 | 0.0020 | 1.0161 0.9842 | |
| Muscle-skeleton | 0.0000 | 0.0153 | 0.0000 undef | |
| Kidney | 0.0017 | 0.0000 | undef 0.0000 | |
| Pancreas | 0.0027 | 0.0000 | undef 0.0000 | |
| Penis | 0.0033 | 0.0000 | undef 0.0000 | |
| Prostate | 0.0030 | 0.0267 | 0.1123 8.9035 | |
| Uterus-endometrium | 0.0000 | 0.0021 | 0.0000 undef | |
| Uterus-myometrium | 0.0068 | 0.0000 | undef 0.0000 | |
| Uterus-general | 0.0000 | 0.0000 | undef undef | |
| Breast hyperplasia | 0.0051 | 0.0000 | undef 0.0000 | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0254 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0020 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 38

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0000 | 0.0000 | undef undef | |
| Small intestine | 0.0000 | 0.0000 | undef undef | |
| Ovary | 0.0000 | 0.0000 | undef undef | |
| Endocrine tissue | 0.0000 | 0.0234 | 0.0000 undef | |
| Gastrointestinal | 0.0000 | 0.0000 | undef undef | |
| Brain | 0.0000 | 0.0000 | undef undef | |
| Hematopoietic | 0.0000 | 0.0000 | undef undef | |
| Skin | 0.0000 | 0.0000 | undef undef | |
| Hepatic | 0.0000 | 0.0000 | undef undef | |
| Heart | 0.0000 | 0.0000 | undef undef | |
| Testicles | 0.0000 | 0.0000 | undef undef | |
| Lung | 0.0000 | 0.0000 | undef undef | |
| Stomach-esophagus | 0.3189 | 0.0153 | 20.7988 | 0.0481 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef | |
| Kidney | 0.0000 | 0.0000 | undef undef | |
| Pancreas | 0.0000 | 0.0000 | undef undef | |
| Penis | 0.0000 | 0.0000 | undef undef | |
| Prostate | 0.0000 | 0.0000 | undef undef | |
| Uterus-endometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-myometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0083 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 39

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0286 | 0.0000 | undef |
| Endocrine tissue | 0.0051 | 0.0075 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0019 | 0.0000 | undef | 0.0000 |
| Brain | 0.0030 | 0.0072 | 0.4114 | 2.4307 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0053 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0117 | 0.4920 | 2.0326 |
| Lung | 0.0021 | 0.0041 | 0.5080 | 1.9684 |
| Stomach-esophagus | 0.0097 | 0.0077 | 1.2605 | 0.7933 |
| Muscle-skeleton | 0.0051 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0054 | 0.0137 | 0.3965 | 2.5219 |
| Pancreas | 0.0033 | 0.0000 | undef | 0.0000 |
| Penis | 0.0090 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0059 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0021 | | | |
| White blood cells | 0.0043 | | | |
| Cervix | 0.0000 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|--------|-------------------------|--------|
| % frequency | | LIBRARIES | |
| | | % frequency | |
| Development | | Breast | |
| Gastrointestinal | | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0070 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0114 |
| Lung | 0.0000 | Skin-muscle | 0.0097 |
| Suprarenal gland | 0.0036 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0062 | Nerves | 0.0020 |
| Prostate | 0.0000 | Prostate | 0.0137 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0291 |

Electronic Northern for SEQ. ID NO.: 40

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0039 | 0.0077 | 0.5085 | 1.9666 |
| Small intestine | 0.0051 | 0.0056 | 0.9074 | 1.1021 |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0030 | 0.0208 | 0.1439 | 6.9489 |
| Gastrointestinal | 0.0102 | 0.0025 | 4.0755 | 0.2454 |
| Brain | 0.0115 | 0.0093 | 1.2425 | 0.8048 |
| Hematopoietic | 0.0044 | 0.0062 | 0.7200 | 1.3890 |
| Skin | 0.0053 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0037 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0021 | 0.0000 | undef | 0.0000 |
| Lung | 0.0058 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0062 | 0.0061 | 1.0161 | 0.9842 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0017 | 0.0120 | 0.1428 | 7.0040 |
| Pancreas | 0.0027 | 0.0068 | 0.3965 | 2.5219 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0030 | 0.0267 | 0.1123 | 8.9035 |
| Uterus-endometrium | 0.0065 | 0.0021 | 3.0709 | 0.3256 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0149 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0035 | | | |
| Cervix | 0.0000 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0111 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0063 | Endocrine tissue | 0.0000 |
| Skin | 0.0039 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0065 |
| Lung | 0.0071 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0164 |
| Kidney | 0.0247 | Lung | 0.0070 |
| Placenta | 0.0061 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0126 | Sensory Organs | 0.0167 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 41

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0031 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0208 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0096 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0230 | 0.0000 | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0118 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 42

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0026 | 0.0000 | undef |
| Breast | 0.0000 | 0.0019 | 0.0000 | undef |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0037 | 0.0010 | 3.5998 | 0.2778 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0052 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0034 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0068 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0064 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0059 | 0.0000 | | |
| Prostate hyperplasia | 0.0000 | 0.0000 | | |
| Seminal vesicle | 0.0000 | 0.0000 | | |
| Sensory organs | 0.0000 | 0.0000 | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast |
| Gastrointestinal | Ovary_n |
| Brain | Ovary_t |
| Hematopoietic | Endocrine tissue |
| Skin | Fetal |
| Hepatic | Gastrointestinal |
| Heart-blood vessels | Hematopoietic |
| Lung | Skin-muscle |
| Suprarenal gland | Testicles |
| Kidney | Lung |
| Placenta | Nerves |
| Prostate | Prostate |
| Sensory organs | Sensory Organs |
| | Uterus_n |

Electronic Northern for SEQ. ID NO.: 43

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|-------|
| Bladder | | | | |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0130 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0235 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|-------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0260 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0118 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 45

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | | | | |
| Breast | 0.0000 | 0.0102 | 0.0000 | undef |
| Small intestine | 0.0090 | 0.0056 | 1.5879 | 0.6298 |
| Ovary | 0.0031 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0060 | 0.0390 | 0.1535 | 6.5146 |
| Gastrointestinal | 0.0034 | 0.0025 | 1.3585 | 0.7361 |
| Brain | 0.0019 | 0.0231 | 0.0828 | 12.0723 |
| Hematopoietic | 0.0000 | 0.0031 | 0.0000 | undef |
| Skin | 0.0080 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0037 | 0.0847 | 0.0433 | 23.0839 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0117 | 0.0000 | undef |
| Stomach-esophagus | 0.0021 | 0.0102 | 0.2032 | 4.9209 |
| Muscle-skeleton | 0.0000 | 0.0077 | 0.0000 | undef |
| Kidney | 0.0017 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0054 | 0.0000 | undef | 0.0000 |
| Penis | 0.0000 | 0.0110 | 0.0000 | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0065 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0229 | 0.0068 | 3.3668 | 0.2970 |
| Breast hyperplasia | 0.0000 | 0.0000 | undef | undef |
| Prostate hyperplasia | 0.0096 | | | |
| Seminal vesicle | 0.0059 | | | |
| Sensory organs | 0.0089 | | | |
| White blood cells | 0.0118 | | | |
| Cervix | 0.0000 | | | |
| | 0.0000 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0057 |
| Lung | 0.0108 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0062 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0491 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0125 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0117 | 0.0102 | 1.1441 | 0.8741 |
| Breast | 0.0090 | 0.0263 | 0.3403 | 2.9389 |
| Small intestine | 0.0184 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0170 | 0.0050 | 3.3962 | 0.2944 |
| Gastrointestinal | 0.0172 | 0.0046 | 3.7275 | 0.2683 |
| Brain | 0.0081 | 0.0216 | 0.3771 | 2.6517 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0065 | 0.7353 | 1.3600 |
| Heart | 0.0117 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0083 | 0.0020 | 4.0643 | 0.2460 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0120 | 0.0060 | 1.9989 | 0.5003 |
| Kidney | 0.0081 | 0.0068 | 1.1896 | 0.8406 |
| Pancreas | 0.0017 | 0.0110 | 0.1496 | 6.6857 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0131 | 0.0021 | 6.1418 | 0.1628 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0030 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0043 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0063 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0171 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0124 | Lung | 0.0000 |
| Placenta | 0.0121 | Nerves | 0.0137 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | |

Electronic Northern for SEQ. ID NO.: 47

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0117 | 0.0051 | 2.2882 | 0.4370 |
| Breast | 0.0090 | 0.0019 | 4.7637 | 0.2099 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0030 | 0.0208 | 0.1439 | 6.9489 |
| Endocrine tissue | 0.0034 | 0.0025 | 1.3585 | 0.7361 |
| Gastrointestinal | 0.0057 | 0.0000 | undef | 0.0000 |
| Brain | 0.0007 | 0.0021 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0053 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0052 | 0.0041 | 1.2701 | 0.7873 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0017 | 0.0180 | 0.0952 | 10.5060 |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0083 | 0.0055 | 1.4957 | 0.6686 |
| Penis | 0.0090 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0064 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0064 | 0.0000 | | |
| Breast hyperplasia | 0.0059 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0118 | | | |
| Sensory organs | 0.0017 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0107 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0020 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0077 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 48

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0156 | 0.0026 | 6.1018 | 0.1639 |
| Breast | 0.0179 | 0.0169 | 1.0586 | 0.9446 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0286 | 0.2093 | 4.7774 |
| Endocrine tissue | 0.0324 | 0.0251 | 1.2906 | 0.7749 |
| Gastrointestinal | 0.0287 | 0.0278 | 1.0354 | 0.9658 |
| Brain | 0.0229 | 0.0164 | 1.3949 | 0.7169 |
| Hematopoietic | 0.0107 | 0.0000 | undef | 0.0000 |
| Skin | 0.0147 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0350 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0117 | 0.4920 | 2.0326 |
| Lung | 0.0239 | 0.0225 | 1.0623 | 0.9414 |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0120 | 0.0060 | 1.9989 | 0.5003 |
| Kidney | 0.0190 | 0.0137 | 1.3878 | 0.7206 |
| Pancreas | 0.0050 | 0.0000 | undef | 0.0000 |
| Penis | 0.0210 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0262 | 0.0085 | 3.0709 | 0.3256 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0068 | 3.3668 | 0.2970 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0160 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0356 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0208 | | | |
| Cervix | 0.0000 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0068 |
| Gastrointestinal | 0.0167 | Ovary_n | 0.1595 |
| Brain | 0.0188 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0082 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0320 | Hematopoietic | 0.0057 |
| Lung | 0.0108 | Skin-muscle | 0.0162 |
| Suprarenal gland | 0.0254 | Testicles | 0.0077 |
| Kidney | 0.0124 | Lung | 0.0164 |
| Placenta | 0.0182 | Nerves | 0.0221 |
| Prostate | 0.0249 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0155 |
| | | Uterus_n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 49

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0051 | 0.7627 | 1.3111 |
| Breast | 0.0038 | 0.0056 | 0.6805 | 1.4694 |
| Small intestine | 0.0031 | 0.0165 | 0.1854 | 5.3946 |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0051 | 0.0025 | 2.0377 | 0.4907 |
| Gastrointestinal | 0.0057 | 0.0139 | 0.4142 | 2.4145 |
| Brain | 0.0037 | 0.0062 | 0.6000 | 1.6668 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0042 | 0.0275 | 0.1542 | 6.4853 |
| Heart | 0.0115 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0021 | 0.0041 | 0.5080 | 1.9684 |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0017 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0109 | 0.0137 | 0.7930 | 1.2610 |
| Kidney | 0.0066 | 0.0055 | 1.1966 | 0.8357 |
| Pancreas | 0.0030 | 0.0000 | undef | 0.0000 |
| Penis | 0.0044 | 0.0064 | 0.6824 | 1.4654 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-myometrium | 0.0051 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0064 | | | |
| Breast hyperplasia | 0.0208 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0017 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0000 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0000 |
| Hematopoietic | Endocrine tissue 0.0000 |
| Skin | Fetal 0.0000 |
| Hepatic | Gastrointestinal 0.0000 |
| Heart-blood vessels | Hematopoietic 0.0065 |
| Lung | Skin-muscle 0.0000 |
| Suprarenal gland | Testicles 0.0000 |
| Kidney | Lung 0.0020 |
| Placenta | Nerves 0.0205 |
| Prostate | Prostate 0.0000 |
| Sensory organs | Sensory Organs 0.0042 |
| | Uterus_n |

Electronic Northern for SEQ. ID NO.: 50

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0078 | 0.0179 | 0.4358 | 2.2944 |
| Breast | 0.0064 | 0.0094 | 0.6805 | 1.4694 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0051 | 0.0075 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0057 | 0.0000 | undef | 0.0000 |
| Brain | 0.0052 | 0.0051 | 1.0079 | 0.9921 |
| Hematopoietic | 0.0080 | 0.0379 | 0.2117 | 4.7230 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0064 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0173 | 0.0117 | 1.4759 | 0.6775 |
| Lung | 0.0073 | 0.0102 | 0.7112 | 1.4060 |
| Stomach-esophagus | 0.0097 | 0.0153 | 0.6303 | 1.5866 |
| Muscle-skeleton | 0.0069 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0137 | 0.1983 | 5.0439 |
| Pancreas | 0.0000 | 0.0055 | 0.0000 | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0131 | 0.0064 | 2.0473 | 0.4885 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0272 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0030 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0043 | | | |
| Cervix | 0.0213 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast |
| Gastrointestinal | Ovary_n |
| Brain | Ovary_t |
| Hematopoietic | Endocrine tissue |
| Skin | Fetal |
| Hepatic | Gastrointestinal |
| Heart-blood vessels | Hematopoietic |
| Lung | Skin-muscle |
| Suprarenal gland | Testicles |
| Kidney | Lung |
| Placenta | Nerves |
| Prostate | Prostate |
| Sensory organs | Sensory Organs |
| | Uterus n |

Electronic Northern for SEQ. ID NO.: 51

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0077 | 0.0000 | undef |
| Breast | 0.0026 | 0.0150 | 0.1701 | 5.8778 |
| Small intestine | 0.0061 | 0.0165 | 0.3707 | 2.6973 |
| Ovary | 0.0030 | 0.0208 | 0.1439 | 6.9489 |
| Endocrine tissue | 0.0119 | 0.0075 | 1.5849 | 0.6309 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0037 | 0.0072 | 0.5143 | 1.9446 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0074 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef |
| Lung | 0.0062 | 0.0061 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0188 | 0.0060 | 3.1411 | 0.3184 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0055 | 0.0000 | undef |
| Penis | 0.0090 | 0.0267 | 0.3369 | 2.9678 |
| Prostate | 0.0153 | 0.0106 | 1.4331 | 0.6978 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-general | 0.0153 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0178 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0026 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | 0.0136 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0079 | Fetal | 0.0052 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0456 |
| Lung | 0.0213 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0072 | Testicles | 0.0077 |
| Kidney | 0.1014 | Lung | 0.0164 |
| Placenta | 0.0000 | Nerves | 0.0040 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 52

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0039 | 0.0102 | 0.3814 | 2.6222 |
| Breast | 0.0179 | 0.0038 | 4.7637 | 0.2099 |
| Small intestine | 0.0092 | 0.0496 | 0.1854 | 5.3946 |
| Ovary | 0.0060 | 0.0260 | 0.2303 | 4.3431 |
| Endocrine tissue | 0.0153 | 0.0251 | 0.6113 | 1.6358 |
| Gastrointestinal | 0.0211 | 0.0463 | 0.4556 | 2.1950 |
| Brain | 0.0155 | 0.0103 | 1.5119 | 0.6614 |
| Hematopoietic | 0.0040 | 0.0758 | 0.0529 | 18.8919 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0388 | 0.0000 | undef |
| Heart | 0.0106 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0177 | 0.0143 | 1.2338 | 0.8105 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0069 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0109 | 0.0274 | 0.3965 | 2.5219 |
| Pancreas | 0.0231 | 0.0221 | 1.0470 | 0.9551 |
| Penis | 0.0090 | 0.0267 | 0.3369 | 2.9678 |
| Prostate | 0.0065 | 0.0106 | 0.6142 | 1.6282 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0204 | 0.3741 | 2.6732 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0256 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0095 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0278 | Breast | 0.0068 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0125 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0142 | Hematopoietic | 0.0057 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0164 |
| Placenta | 0.0061 | Nerves | 0.0060 |
| Prostate | 0.0499 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0234 | 0.0153 | 1.5254 | 0.6555 |
| Breast | 0.0115 | 0.0113 | 1.0208 | 0.9796 |
| Small intestine | 0.0092 | 0.0165 | 0.5561 | 1.7982 |
| Ovary | 0.0090 | 0.0286 | 0.3140 | 3.1849 |
| Endocrine tissue | 0.0102 | 0.0125 | 0.8151 | 1.2268 |
| Gastrointestinal | 0.0230 | 0.0278 | 0.8283 | 1.2072 |
| Brain | 0.0148 | 0.0144 | 1.0285 | 0.9723 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0106 | 0.0275 | 0.3855 | 2.5941 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0125 | 0.0123 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0137 | 0.0120 | 1.1422 | 0.8755 |
| Kidney | 0.0136 | 0.0274 | 0.4956 | 2.0176 |
| Pancreas | 0.0099 | 0.0110 | 0.8974 | 1.1143 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0109 | 0.0192 | 0.5687 | 1.7585 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0136 | 0.5611 | 1.7821 |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0087 | | | |
| Cervix | 0.0000 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | | % frequency |
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0139 | Ovary_n | 0.1595 |
| Brain | 0.0083 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0063 | Endocrine tissue | 0.0000 |
| Skin | 0.0039 | Fetal | 0.0017 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0520 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0181 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0020 |
| Placenta | 0.0371 | Nerves | 0.0000 |
| Prostate | 0.0061 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | 0.0126 | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 54

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0039 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0038 | 0.3403 | 2.9389 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0025 | 1.3585 | 0.7361 |
| Gastrointestinal | 0.0019 | 0.0000 | undef | 0.0000 |
| Brain | 0.0052 | 0.0051 | 1.0079 | 0.9921 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0032 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0031 | 0.0020 | 1.5241 | 0.6561 |
| Lung | 0.0097 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0017 | 0.0060 | 0.2856 | 3.5020 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0017 | 0.0221 | 0.0748 | 13.3713 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0043 | 0.0000 | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0032 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0068 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0082 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0114 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0164 |
| Placenta | 0.0121 | Nerves | 0.0060 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 55

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0039 | 0.0204 | 0.1907 | 5.2444 |
| Breast | 0.0141 | 0.0150 | 0.9357 | 1.0687 |
| Small intestine | 0.0061 | 0.0496 | 0.1236 | 8.0920 |
| Ovary | 0.0120 | 0.0364 | 0.3289 | 3.0402 |
| Endocrine tissue | 0.0085 | 0.0050 | 1.6981 | 0.5889 |
| Gastrointestinal | 0.0096 | 0.0046 | 2.0708 | 0.4829 |
| Brain | 0.0140 | 0.0185 | 0.7600 | 1.3159 |
| Hematopoietic | 0.0067 | 0.0000 | undef | 0.0000 |
| Skin | 0.0294 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0065 | 1.4706 | 0.6800 |
| Heart | 0.0138 | 0.0412 | 0.3341 | 2.9932 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0156 | 0.0164 | 0.9526 | 1.0498 |
| Stomach-esophagus | 0.0193 | 0.0307 | 0.6303 | 1.5866 |
| Muscle-skeleton | 0.0103 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0331 | 0.0499 | 20.0570 |
| Penis | 0.0120 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0174 | 0.0234 | 0.7445 | 1.3433 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0136 | 1.6834 | 0.5940 |
| Uterus-general | 0.0051 | 0.0954 | 0.0534 | 18.7357 |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0238 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0139 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0222 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0304 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0047 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0488 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0114 |
| Lung | 0.0072 | Skin-muscle | 0.0162 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0303 | Nerves | 0.0090 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0126 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0250 |

Electronic Northern for SEQ. ID NO.: 56

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0078 | 0.0153 | 0.5085 | 1.9666 |
| Breast | 0.0077 | 0.0132 | 0.5833 | 1.7144 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0234 | 0.1279 | 7.8175 |
| Endocrine tissue | 0.0085 | 0.0025 | 3.3962 | 0.2944 |
| Gastrointestinal | 0.0019 | 0.0093 | 0.2071 | 4.8289 |
| Brain | 0.0022 | 0.0072 | 0.3086 | 3.2409 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0201 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0468 | 0.0000 | undef |
| Lung | 0.0031 | 0.0102 | 0.3048 | 3.2806 |
| Stomach-esophagus | 0.0193 | 0.0153 | 1.2605 | 0.7933 |
| Muscle-skeleton | 0.0120 | 0.0120 | 0.9994 | 1.0006 |
| Kidney | 0.0000 | 0.0068 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0276 | 0.0000 | undef |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0085 | 0.7677 | 1.3026 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0152 | 0.0068 | 2.2445 | 0.4455 |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0182 | | | |
| Cervix | 0.0213 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------------|---|
| Development | Breast 0.0068 |
| Gastrointestinal 0.0000 | Ovary_n 0.0000 |
| Brain 0.0028 | Ovary_t 0.0152 |
| Hematopoietic 0.0063 | Endocrine tissue 0.0245 |
| Skin 0.0039 | Fetal 0.0012 |
| Hepatic 0.0000 | Gastrointestinal 0.0000 |
| Heart-blood vessels 0.0000 | Hematopoietic 0.0000 |
| Lung 0.0178 | Skin-muscle 0.0065 |
| Suprarenal gland 0.0108 | Testicles 0.0000 |
| Kidney 0.0000 | Lung 0.0246 |
| Placenta 0.0124 | Nerves 0.0060 |
| Prostate 0.0061 | Prostate 0.0000 |
| Sensory organs 0.0000 | Sensory Organs 0.0000 |
| | Uterus_n 0.0042 |

Electronic Northern for SEQ. ID NO.: 57

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0026 | 1.5254 | 0.6555 |
| Breast | 0.0128 | 0.0150 | 0.8507 | 1.1756 |
| Small intestine | 0.0061 | 0.0165 | 0.3707 | 2.6973 |
| Ovary | 0.0030 | 0.0208 | 0.1439 | 6.9489 |
| Endocrine tissue | 0.0051 | 0.0226 | 0.2264 | 4.4166 |
| Gastrointestinal | 0.0077 | 0.0000 | undef | 0.0000 |
| Brain | 0.0074 | 0.0103 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0174 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0085 | 0.0275 | 0.3084 | 3.2426 |
| Testicles | 0.0115 | 0.0000 | undef | 0.0000 |
| Lung | 0.0062 | 0.0102 | 0.6096 | 1.6403 |
| Stomach-esophagus | 0.0000 | 0.0307 | 0.0000 | undef |
| Muscle-skeleton | 0.0120 | 0.0060 | 1.9989 | 0.5003 |
| Kidney | 0.0217 | 0.0068 | 3.1722 | 0.3152 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0018 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0085 | 0.5118 | 1.9538 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0272 | 0.2806 | 3.5642 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0139 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0278 | Breast | 0.0068 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0188 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0076 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0142 | Hematopoietic | 0.0000 |
| Lung | 0.0145 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0124 | Lung | 0.0120 |
| Placenta | 0.0000 | Nerves | 0.0274 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | |

Electronic Northern for SEQ. ID NO.: 58

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0585 | 0.0332 | 1.7601 | 0.5681 |
| Breast | 0.0230 | 0.0132 | 1.7499 | 0.5715 |
| Small intestine | 0.0153 | 0.0827 | 0.1854 | 5.3946 |
| Ovary | 0.0150 | 0.0546 | 0.2741 | 3.6482 |
| Endocrine tissue | 0.0136 | 0.0150 | 0.9057 | 1.1042 |
| Gastrointestinal | 0.0192 | 0.0416 | 0.4602 | 2.1730 |
| Brain | 0.0163 | 0.0277 | 0.5866 | 1.7046 |
| Hematopoietic | 0.0374 | 0.0379 | 0.9881 | 1.0121 |
| Skin | 0.0404 | 0.0847 | 0.4765 | 2.0985 |
| Hepatic | 0.0143 | 0.0388 | 0.3676 | 2.7200 |
| Heart | 0.0297 | 0.0412 | 0.7196 | 1.3897 |
| Testicles | 0.0863 | 0.1169 | 0.7380 | 1.3551 |
| Lung | 0.0364 | 0.0266 | 1.3678 | 0.7311 |
| Stomach-esophagus | 0.0290 | 0.0767 | 0.3782 | 2.6444 |
| Muscle-skeleton | 0.0411 | 0.0360 | 1.1422 | 0.8755 |
| Kidney | 0.0190 | 0.0137 | 1.3878 | 0.7206 |
| Pancreas | 0.0132 | 0.0497 | 0.2659 | 3.7607 |
| Penis | 0.0359 | 0.0800 | 0.4493 | 2.2259 |
| Prostate | 0.0262 | 0.0128 | 2.0473 | 0.4885 |
| Uterus-endometrium | 0.0338 | 0.0528 | 0.6402 | 1.5621 |
| Uterus-myometrium | 0.0229 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0178 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0251 | | | |
| Cervix | 0.0106 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0000 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0000 |
| Hematopoietic | Endocrine tissue 0.0000 |
| Skin | Fetal 0.0093 |
| Hepatic | Gastrointestinal 0.0366 |
| Heart-blood vessels | Hematopoietic 0.0057 |
| Lung | Skin-muscle 0.0389 |
| Suprarenal gland | Testicles 0.0154 |
| Kidney | Lung 0.0491 |
| Placenta | Nerves 0.0120 |
| Prostate | Prostate 0.0068 |
| Sensory organs | Sensory Organs 0.0077 |
| | Uterus_n 0.0250 |

Electronic Northern for SEQ. ID NO.: 59

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0117 | 0.0102 | 1.1441 | 0.8741 |
| Breast | 0.0038 | 0.0056 | 0.6805 | 1.4694 |
| Small intestine | 0.0031 | 0.0165 | 0.1854 | 5.3946 |
| Ovary | 0.0060 | 0.0390 | 0.1535 | 6.5146 |
| Endocrine tissue | 0.0102 | 0.0251 | 0.4075 | 2.4537 |
| Gastrointestinal | 0.0077 | 0.0093 | 0.8283 | 1.2072 |
| Brain | 0.0140 | 0.0082 | 1.7099 | 0.5848 |
| Hematopoietic | 0.0053 | 0.1515 | 0.0353 | 28.3379 |
| Skin | 0.0220 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0148 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0104 | 0.0184 | 0.5645 | 1.7715 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0051 | 0.0180 | 0.2856 | 3.5020 |
| Kidney | 0.0109 | 0.0137 | 0.7930 | 1.2610 |
| Pancreas | 0.0099 | 0.0110 | 0.8974 | 1.1143 |
| Penis | 0.0180 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0043 | 0.5118 | 1.9538 |
| Uterus-endometrium | 0.0270 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0192 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0061 | | | |
| Cervix | 0.0213 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0835 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0375 | Ovary_t | 0.0203 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0213 | Hematopoietic | 0.0000 |
| Lung | 0.0108 | Skin-muscle | 0.0162 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0246 |
| Placenta | 0.0182 | Nerves | 0.0241 |
| Prostate | 0.0249 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0230 | 0.0000 | undef |
| Breast | 0.0000 | 0.0150 | 0.0000 | undef |
| Small intestine | 0.0675 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0208 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0153 | 0.0139 | 1.1045 | 0.9054 |
| Brain | 0.0022 | 0.0154 | 0.1440 | 6.9448 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0323 | 0.0000 | undef |
| Heart | 0.0064 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0020 | 0.0000 | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 6.3239 | 0.7179 | 8.8087 | 0.1135 |
| Pancreas | 0.0030 | 0.0000 | undef | 0.0000 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0089 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0106 | | | |
| Sensory organs | | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.2721 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0354 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0017 |
| Hepatic | 0.0000 | Gastrointestinal | 0.2685 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0097 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | | Sensory Organs | 0.0083 |
| | | Uterus n | |

Electronic Northern for SEQ. ID NO.: 65

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0039 | 0.0077 | 0.5085 | 1.9666 |
| Breast | 0.0064 | 0.0075 | 0.8507 | 1.1756 |
| Small intestine | 0.0245 | 0.0165 | 1.4830 | 0.6743 |
| Ovary | 0.0090 | 0.0520 | 0.1727 | 5.7908 |
| Endocrine tissue | 0.0085 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0153 | 0.0324 | 0.4733 | 2.1127 |
| Brain | 0.0044 | 0.0123 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0381 | 0.0970 | 0.3922 | 2.5500 |
| Heart | 0.0074 | 0.0137 | 0.5397 | 1.8529 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0052 | 0.0082 | 0.6350 | 1.5747 |
| Stomach-esophagus | 0.0000 | 0.0230 | 0.0000 | undef |
| Muscle-skeleton | 0.0086 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0163 | 0.0616 | 0.2643 | 3.7829 |
| Pancreas | 0.0396 | 0.0055 | 7.1795 | 0.1393 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0106 | 0.6142 | 1.6282 |
| Uterus-endometrium | 0.0000 | 0.0528 | 0.0000 | undef |
| Uterus-myometrium | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-general | 0.0153 | 0.2863 | 0.0534 | 18.7357 |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0043 | | | |
| Cervix | 0.0319 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0222 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0122 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0228 |
| Lung | 0.0036 | Skin-muscle | 0.0162 |
| Suprarenal gland | 0.0254 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0082 |
| Placenta | 0.0242 | Nerves | 0.0010 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0250 |

Electronic Northern for SEQ. ID NO.: 67

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0102 | 0.3814 | 2.6222 |
| Breast | 0.0026 | 0.0169 | 0.1512 | 6.6125 |
| Small intestine | 0.0092 | 0.0165 | 0.5561 | 1.7982 |
| Ovary | 0.0060 | 0.0260 | 0.2303 | 4.3431 |
| Endocrine tissue | 0.0034 | 0.0075 | 0.4528 | 2.2083 |
| Gastrointestinal | 0.0057 | 0.0185 | 0.3106 | 3.2193 |
| Brain | 0.0044 | 0.0062 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0094 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0129 | 0.0000 | undef |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0115 | 0.0000 | undef | 0.0000 |
| Lung | 0.0031 | 0.0102 | 0.3048 | 3.2806 |
| Stomach-esophagus | 0.0097 | 0.0153 | 0.6303 | 1.5866 |
| Muscle-skeleton | 0.0017 | 0.0060 | 0.2856 | 3.5020 |
| Kidney | 0.0081 | 0.0068 | 1.1896 | 0.8406 |
| Pancreas | 0.0050 | 0.0055 | 0.8974 | 1.1143 |
| Penis | 0.0120 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0085 | 0.2559 | 3.9077 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0061 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0272 |
| Brain | 0.0056 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0188 | Endocrine tissue | 0.0000 |
| Skin | 0.0157 | | 0.0245 |
| Hepatic | 0.0000 | Fetal | 0.0169 |
| Heart-blood vessels | 0.0000 | Gastrointestinal | 0.0000 |
| Lung | 0.0000 | Hematopoietic | 0.0171 |
| Suprarenal gland | 0.0036 | Skin-muscle | 0.0000 |
| Kidney | 0.0000 | Testicles | 0.0000 |
| Placenta | 0.0000 | Lung | 0.0328 |
| Prostate | 0.0121 | Nerves | 0.0080 |
| Sensory organs | 0.0000 | Prostate | 0.0000 |
| | 0.0126 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0125 |

Electronic Northern for SEQ. ID NO.: 69

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T T/N | |
|----------------------|-----------------------|----------------------|------------------------|--------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0025 | 0.0000 | undef |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0007 | 0.0021 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0288 | 0.0000 | undef | 0.0000 |
| Lung | 0.0031 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0050 | 0.0055 | 0.8974 | 1.1143 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0102 | 0.0954 | 0.1067 | 9.3678 |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0017 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS % frequency | | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|----------------------|--------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.1595 |
| Brain | 0.0000 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0029 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0342 |
| Lung | 0.0108 | Skin-muscle | 0.0097 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0020 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 70

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0078 | 0.0000 | undef | 0.0000 |
| Breast | 0.0077 | 0.0094 | 0.8166 | 1.2245 |
| Small intestine | 0.0123 | 0.0165 | 0.7415 | 1.3487 |
| Ovary | 0.0060 | 0.0260 | 0.2303 | 4.3431 |
| Endocrine tissue | 0.0324 | 0.0075 | 4.3019 | 0.2325 |
| Gastrointestinal | 0.0134 | 0.0093 | 1.4496 | 0.6898 |
| Brain | 0.0111 | 0.0051 | 2.1599 | 0.4630 |
| Hematopoietic | 0.0040 | 0.0379 | 0.1059 | 9.4460 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0065 | 1.4706 | 0.6800 |
| Heart | 0.0148 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0135 | 0.0102 | 1.3209 | 0.7571 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0060 | 0.2856 | 3.5020 |
| Kidney | 0.0109 | 0.0068 | 1.5861 | 0.6305 |
| Pancreas | 0.0099 | 0.0055 | 1.7949 | 0.5571 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0109 | 0.0085 | 1.2795 | 0.7815 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0149 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0130 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0056 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0063 | Endocrine tissue | 0.0101 |
| Skin | 0.0118 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0041 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0142 | Skin-muscle | 0.0057 |
| Suprarenal gland | 0.0072 | Testicles | 0.0097 |
| Kidney | 0.0000 | Lung | 0.0154 |
| Placenta | 0.0000 | Nerves | 0.0164 |
| Prostate | 0.0182 | Prostate | 0.0070 |
| Sensory organs | 0.0249 | Sensory Organs | 0.0137 |
| | 0.0126 | Uterus_n | 0.0000 |
| | | | 0.0083 |

Electronic Northern for SEQ. ID NO.: 72

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.1053 | 0.0895 | 1.1768 | 0.8498 |
| Breast | 0.0652 | 0.0846 | 0.7713 | 1.2966 |
| Small intestine | 0.1073 | 0.0992 | 1.0813 | 0.9248 |
| Ovary | 0.0629 | 0.1353 | 0.4649 | 2.1509 |
| Endocrine tissue | 0.0579 | 0.0451 | 1.2830 | 0.7794 |
| Gastrointestinal | 0.1379 | 0.2220 | 0.6213 | 1.6096 |
| Brain | 0.0702 | 0.0534 | 1.3153 | 0.7603 |
| Hematopoietic | 0.1056 | 0.1136 | 0.9293 | 1.0761 |
| Skin | 0.0587 | 0.0847 | 0.6931 | 1.4427 |
| Hepatic | 0.0285 | 0.1035 | 0.2757 | 3.6266 |
| Heart | 0.1293 | 0.0412 | 3.1353 | 0.3189 |
| Testicles | 0.0403 | 0.1754 | 0.2296 | 4.3556 |
| Lung | 0.0914 | 0.1063 | 0.8598 | 1.1631 |
| Stomach-esophagus | 0.0387 | 0.1840 | 0.2101 | 4.7599 |
| Muscle-skeleton | 0.0548 | 0.1260 | 0.4351 | 2.2982 |
| Kidney | 0.0814 | 0.1438 | 0.5665 | 1.7654 |
| Pancreas | 0.0363 | 0.1878 | 0.1936 | 5.1662 |
| Penis | 0.1138 | 0.0800 | 1.4227 | 0.7029 |
| Prostate | 0.0697 | 0.0958 | 0.7279 | 1.3738 |
| Uterus-endometrium | 0.1824 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0838 | 0.0951 | 0.8818 | 1.1341 |
| Uterus-general | 0.1171 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0671 | | | |
| Prostate hyperplasia | 0.0922 | | | |
| Seminal vesicle | 0.0712 | | | |
| Sensory organs | 0.0706 | | | |
| White blood cells | 0.1448 | | | |
| Cervix | 0.1810 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0557 | Breast | 0.0340 |
| Gastrointestinal | 0.1083 | Ovary_n | 0.0000 |
| Brain | 0.0500 | Ovary_t | 0.0253 |
| Hematopoietic | 0.0944 | Endocrine tissue | 0.0000 |
| Skin | 0.2513 | Fetal | 0.0163 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0712 | Hematopoietic | 0.0000 |
| Lung | 0.1409 | Skin-muscle | 0.0292 |
| Suprarenal gland | 0.0507 | Testicles | 0.0077 |
| Kidney | 0.1297 | Lung | 0.0246 |
| Placenta | 0.0545 | Nerves | 0.0090 |
| Prostate | 0.0499 | Prostate | 0.0274 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 73

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0663 | 0.0895 | 0.7409 | 1.3497 |
| Breast | 0.0371 | 0.0489 | 0.7591 | 1.3174 |
| Small intestine | 0.0766 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0270 | 0.0754 | 0.3573 | 2.7989 |
| Endocrine tissue | 0.0170 | 0.0326 | 0.5225 | 1.9139 |
| Gastrointestinal | 0.0805 | 0.0833 | 0.9664 | 1.0348 |
| Brain | 0.0177 | 0.0390 | 0.4547 | 2.1992 |
| Hematopoietic | 0.0896 | 0.0758 | 1.1822 | 0.8459 |
| Skin | 0.0551 | 0.1695 | 0.3249 | 3.0779 |
| Hepatic | 0.0238 | 0.0776 | 0.3064 | 3.2640 |
| Heart | 0.0604 | 0.1237 | 0.4883 | 2.0480 |
| Testicles | 0.0288 | 0.0702 | 0.4100 | 2.4391 |
| Lung | 0.0519 | 0.0429 | 1.2096 | 0.8267 |
| Stomach-esophagus | 0.0676 | 0.0843 | 0.8022 | 1.2466 |
| Muscle-skeleton | 0.0223 | 0.0240 | 0.9280 | 1.0775 |
| Kidney | 0.0353 | 0.0548 | 0.6443 | 1.5520 |
| Pancreas | 0.0132 | 0.0773 | 0.1709 | 5.8500 |
| Penis | 0.0838 | 0.0533 | 1.5724 | 0.6360 |
| Prostate | 0.0567 | 0.0255 | 2.2179 | 0.4509 |
| Uterus-endometrium | 0.0946 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0762 | 0.0679 | 1.1223 | 0.8911 |
| Uterus-general | 0.0407 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0192 | | | |
| Prostate hyperplasia | 0.0505 | | | |
| Seminal vesicle | 0.0445 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0772 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0139 | Breast | 0.0272 |
| Gastrointestinal | 0.0305 | Ovary_n | 0.0000 |
| Brain | 0.0313 | Ovary_t | 0.1468 |
| Hematopoietic | 0.0393 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0105 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0366 |
| Heart-blood vessels | 0.0285 | Hematopoietic | 0.0057 |
| Lung | 0.0145 | Skin-muscle | 0.0292 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0679 | Lung | 0.0328 |
| Placenta | 0.0364 | Nerves | 0.0040 |
| Prostate | 0.0997 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0250 |

Electronic Northern for SEQ. ID NO.: 74

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0234 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0468 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0110 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0353 | 0.0164 | 2.1591 | 0.4631 |
| Lung | 0.1836 | 0.1227 | 1.4969 | 0.6681 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0050 | 0.0221 | 0.2244 | 4.4571 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0022 | 0.0128 | 0.1706 | 5.8615 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.1246 | 0.0000 | undef | undef |
| Prostate hyperplasia | 0.0000 | 0.0000 | undef | undef |
| Seminal vesicle | 0.0000 | 0.0000 | undef | undef |
| Sensory organs | 0.0000 | 0.0000 | undef | undef |
| White blood cells | 0.0000 | 0.0000 | undef | undef |
| Cervix | 0.0000 | 0.0000 | undef | undef |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 76

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0000 | 0.0077 | 0.0000 | undef |
| Breast | 0.0026 | 0.0301 | 0.0851 | 11.7556 |
| Small intestine | 0.0000 | 0.0331 | 0.0000 | undef |
| Ovary | 0.0030 | 0.0728 | 0.0411 | 24.3213 |
| Endocrine tissue | 0.0000 | 0.0100 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0046 | 0.0000 | undef |
| Brain | 0.0510 | 0.0596 | 0.8565 | 1.1675 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.1695 | 0.0217 | 46.1678 |
| Hepatic | 0.0523 | 0.1747 | 0.2996 | 3.3382 |
| Heart | 0.0138 | 0.0137 | 1.0023 | 0.9977 |
| Testicles | 0.0000 | 0.0935 | 0.0000 | undef |
| Lung | 0.0073 | 0.0818 | 0.0889 | 11.2478 |
| Stomach-esophagus | 0.0000 | 0.0230 | 0.0000 | undef |
| Muscle-skeleton | 0.0240 | 0.2760 | 0.0869 | 11.5066 |
| Kidney | 0.3910 | 0.4108 | 0.9516 | 1.0508 |
| Pancreas | 0.1123 | 0.0387 | 2.9060 | 0.3441 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0021 | 0.0000 | undef |
| Uterus-endometrium | 0.0068 | 0.2111 | 0.0320 | 31.2422 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.1908 | 0.0267 | 37.4714 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.1838 | | | |
| Cervix | 0.0000 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0696 | Breast | 0.0000 |
| Gastrointestinal | 0.0194 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0128 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0107 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0254 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0164 |
| Placenta | 0.2302 | Nerves | 0.0231 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.1632 | Sensory Organs | 0.0310 |
| | | Uterus_n | 0.0000 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0156 | 0.0153 | 1.0170 | 0.9833 |
| Breast | 0.0090 | 0.0244 | 0.3664 | 2.7290 |
| Small intestine | 0.0123 | 0.0496 | 0.2472 | 4.0460 |
| Ovary | 0.0090 | 0.0338 | 0.2657 | 3.7640 |
| Endocrine tissue | 0.0136 | 0.0226 | 0.6038 | 1.6562 |
| Gastrointestinal | 0.0172 | 0.0324 | 0.5325 | 1.8779 |
| Brain | 0.0044 | 0.0216 | 0.2057 | 4.8614 |
| Hematopoietic | 0.0254 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0065 | 0.7353 | 1.3600 |
| Heart | 0.0170 | 0.0137 | 1.2336 | 0.8107 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0073 | 0.0286 | 0.2540 | 3.9367 |
| Stomach-esophagus | 0.0000 | 0.0307 | 0.0000 | undef |
| Muscle-skeleton | 0.0051 | 0.0180 | 0.2856 | 3.5020 |
| Kidney | 0.0190 | 0.0068 | 2.7756 | 0.3603 |
| Pancreas | 0.0083 | 0.0110 | 0.7479 | 1.3371 |
| Penis | 0.0120 | 0.0267 | 0.4493 | 2.2259 |
| Prostate | 0.0131 | 0.0106 | 1.2284 | 0.8141 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0136 | 0.5611 | 1.7821 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0192 | | | |
| Prostate hyperplasia | 0.0030 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0113 | | | |
| Cervix | 0.0213 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0250 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0118 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0256 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0178 | Hematopoietic | 0.0000 |
| Lung | 0.0145 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0000 | Testicles | 0.0309 |
| Kidney | 0.0371 | Lung | 0.0164 |
| Placenta | 0.0061 | Nerves | 0.0100 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0377 | Sensory Organs | 0.1084 |
| | | Uterus n | 0.0250 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0273 | 0.0332 | 0.8214 | 1.2174 |
| Breast | 0.0230 | 0.0188 | 1.2250 | 0.8164 |
| Small intestine | 0.0276 | 0.0331 | 0.8342 | 1.1988 |
| Ovary | 0.0210 | 0.0650 | 0.3224 | 3.1022 |
| Endocrine tissue | 0.0238 | 0.0276 | 0.8645 | 1.1567 |
| Gastrointestinal | 0.0172 | 0.0463 | 0.3728 | 2.6827 |
| Brain | 0.0118 | 0.0144 | 0.8228 | 1.2153 |
| Hematopoietic | 0.0214 | 0.0379 | 0.5646 | 1.7711 |
| Skin | 0.0147 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0259 | 0.1838 | 5.4400 |
| Heart | 0.0540 | 0.0550 | 0.9830 | 1.0173 |
| Testicles | 0.0173 | 0.0585 | 0.2952 | 3.3877 |
| Lung | 0.0322 | 0.0450 | 0.7159 | 1.3969 |
| Stomach-esophagus | 0.0290 | 0.0077 | 3.7816 | 0.2644 |
| Muscle-skeleton | 0.0240 | 0.0600 | 0.3998 | 2.5014 |
| Kidney | 0.0353 | 0.0548 | 0.6443 | 1.5520 |
| Pancreas | 0.0165 | 0.0221 | 0.7479 | 1.3371 |
| Penis | 0.0150 | 0.0267 | 0.5616 | 1.7807 |
| Prostate | 0.0240 | 0.0405 | 0.5926 | 1.6874 |
| Uterus-endometrium | 0.0270 | 0.1055 | 0.2561 | 3.9053 |
| Uterus-myometrium | 0.0381 | 0.0068 | 5.6113 | 0.1782 |
| Uterus-general | 0.0051 | 0.1908 | 0.0267 | 37.4714 |
| Breast hyperplasia | 0.0224 | | | |
| Prostate hyperplasia | 0.0297 | | | |
| Seminal vesicle | 0.0534 | | | |
| Sensory organs | 0.0588 | | | |
| White blood cells | 0.0234 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0557 | Breast | 0.0136 |
| Gastrointestinal | 0.0083 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0256 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0142 | Hematopoietic | 0.0000 |
| Lung | 0.0253 | Skin-muscle | 0.0583 |
| Suprarenal gland | 0.0507 | Testicles | 0.0231 |
| Kidney | 0.0432 | Lung | 0.0491 |
| Placenta | 0.0303 | Nerves | 0.0221 |
| Prostate | 0.1247 | Prostate | 0.0821 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0416 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0075 | 0.3403 | 2.9389 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0182 | 0.1645 | 6.0803 |
| Endocrine tissue | 0.0017 | 0.0025 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0000 | 0.0139 | 0.0000 | undef |
| Brain | 0.0044 | 0.0041 | 1.0799 | 0.9260 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0117 | 0.4920 | 2.0326 |
| Lung | 0.0010 | 0.0020 | 0.5080 | 1.9684 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0033 | 0.0055 | 0.5983 | 1.6714 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0044 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0017 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0093 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0114 |
| Lung | 0.0254 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0062 | Testicles | 0.0309 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0060 |
| Prostate | 0.0126 | Prostate | 0.0068 |
| Sensory organs | | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 81

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0039 | 0.0128 | 0.3051 | 3.2777 |
| Breast | 0.0141 | 0.0150 | 0.9357 | 1.0687 |
| Small intestine | 0.0153 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0416 | 0.2159 | 4.6326 |
| Endocrine tissue | 0.0119 | 0.0176 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0096 | 0.0139 | 0.6903 | 1.4487 |
| Brain | 0.0126 | 0.0031 | 4.0798 | 0.2451 |
| Hematopoietic | 0.0080 | 0.1136 | 0.0706 | 14.1689 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0065 | 0.7353 | 1.3600 |
| Heart | 0.0191 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0173 | 0.0117 | 1.4759 | 0.6775 |
| Lung | 0.0104 | 0.0164 | 0.6350 | 1.5747 |
| Stomach-esophagus | 0.0000 | 0.0153 | 0.0000 | undef |
| Muscle-skeleton | 0.0069 | 0.0120 | 0.5711 | 1.7510 |
| Kidney | 0.0109 | 0.0137 | 0.7930 | 1.2610 |
| Pancreas | 0.0033 | 0.0000 | undef | 0.0000 |
| Penis | 0.0090 | 0.0267 | 0.3369 | 2.9678 |
| Prostate | 0.0131 | 0.0021 | 6.1418 | 0.1628 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0136 | 0.0000 | undef |
| Uterus-general | 0.0128 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0119 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0104 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0278 | Breast | 0.0000 |
| Gastrointestinal | 0.0111 | Ovary_n | 0.1595 |
| Brain | 0.0250 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0157 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0070 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0285 | Hematopoietic | 0.0057 |
| Lung | 0.0108 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0254 | Testicles | 0.0231 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0191 |
| Prostate | 0.0377 | Prostate | 0.0068 |
| Sensory organs | | Sensory Organs | 0.0155 |
| | | Uterus_n | 0.0250 |

Electronic Northern for SEQ. ID NO.: 82

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0351 | 0.0435 | 0.8076 | 1.2383 |
| Breast | 0.0576 | 0.0489 | 1.1778 | 0.8490 |
| Small intestine | 0.0337 | 0.0165 | 2.0391 | 0.4904 |
| Ovary | 0.0659 | 0.1353 | 0.4871 | 2.0531 |
| Endocrine tissue | 0.0801 | 0.0878 | 0.9121 | 1.0963 |
| Gastrointestinal | 0.0441 | 0.1203 | 0.3664 | 2.7294 |
| Brain | 0.1072 | 0.0298 | 3.5998 | 0.2778 |
| Hematopoietic | 0.0201 | 0.1515 | 0.1323 | 7.5568 |
| Skin | 0.0661 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0428 | 0.0582 | 0.7353 | 1.3600 |
| Heart | 0.0572 | 0.0687 | 0.8327 | 1.2010 |
| Testicles | 0.0460 | 0.1988 | 0.2315 | 4.3193 |
| Lung | 0.0416 | 0.0634 | 0.6555 | 1.5255 |
| Stomach-esophagus | 0.0290 | 0.0613 | 0.4727 | 2.1155 |
| Muscle-skeleton | 0.0360 | 0.0180 | 1.9989 | 0.5003 |
| Kidney | 0.0489 | 0.0411 | 1.1896 | 0.8406 |
| Pancreas | 0.1371 | 0.0552 | 2.4829 | 0.4028 |
| Penis | 0.0479 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0741 | 0.0426 | 1.7402 | 0.5747 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0534 | 0.0475 | 1.1223 | 0.8911 |
| Uterus-general | 0.0407 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0639 | | | |
| Prostate hyperplasia | 0.0476 | | | |
| Seminal vesicle | 0.0623 | | | |
| Sensory organs | 0.0588 | | | |
| White blood cells | 0.0546 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0696 | Breast | 0.0068 |
| Gastrointestinal | 0.1971 | Ovary_n | 0.0000 |
| Brain | 0.0500 | Ovary_t | 0.0304 |
| Hematopoietic | 0.0551 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0262 |
| Hepatic | 0.1040 | Gastrointestinal | 0.1220 |
| Heart-blood vessels | 0.0427 | Hematopoietic | 0.0285 |
| Lung | 0.1120 | Skin-muscle | 0.0356 |
| Suprarenal gland | 0.1521 | Testicles | 0.0309 |
| Kidney | 0.0309 | Lung | 0.2211 |
| Placenta | 0.1212 | Nerves | 0.0502 |
| Prostate | 0.0748 | Prostate | 0.0615 |
| Sensory organs | 0.0628 | Sensory Organs | 0.1471 |
| | | Uterus_n | 0.0125 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0156 | 0.0077 | 2.0339 | 0.4917 |
| Breast | 0.0307 | 0.0169 | 1.8147 | 0.5510 |
| Small intestine | 0.0123 | 0.0165 | 0.7415 | 1.3487 |
| Ovary | 0.0120 | 0.0416 | 0.2878 | 3.4745 |
| Endocrine tissue | 0.0273 | 0.0176 | 1.5526 | 0.6441 |
| Gastrointestinal | 0.0153 | 0.0324 | 0.4733 | 2.1127 |
| Brain | 0.0192 | 0.0154 | 1.2479 | 0.8013 |
| Hematopoietic | 0.0147 | 0.0379 | 0.3882 | 2.5762 |
| Skin | 0.0220 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0238 | 0.0065 | 3.6765 | 0.2720 |
| Heart | 0.0170 | 0.0137 | 1.2336 | 0.8107 |
| Testicles | 0.0230 | 0.0234 | 0.9839 | 1.0163 |
| Lung | 0.0177 | 0.0204 | 0.8637 | 1.1579 |
| | 0.0000 | 0.0153 | 0.0000 | undef |
| Stomach-esophagus | 0.0154 | 0.0060 | 2.5700 | 0.3891 |
| Muscle-skeleton | 0.0190 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0132 | 0.0166 | 0.7977 | 1.2536 |
| Pancreas | 0.0240 | 0.0000 | undef | 0.0000 |
| Penis | 0.0109 | 0.0106 | 1.0236 | 0.9769 |
| Prostate | 0.0338 | 0.0000 | undef | 0.0000 |
| | 0.0305 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0204 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0416 | | | |
| Uterus-general | 0.0208 | | | |
| Breast hyperplasia | 0.0178 | | | |
| Prostate hyperplasia | 0.0235 | | | |
| Seminal vesicle | 0.0087 | | | |
| Sensory organs | 0.0213 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | | % frequency |
| Development | | Breast | 0.0068 |
| Gastrointestinal | 0.0278 | Ovary_n | 0.1595 |
| Brain | 0.0056 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0438 | Endocrine tissue | 0.0000 |
| Skin | 0.0039 | Fetal | 0.0111 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0427 | Skin-muscle | 0.0097 |
| Suprarenal gland | 0.0145 | Testicles | 0.0000 |
| Kidney | 0.0254 | Lung | 0.0231 |
| Placenta | 0.0062 | Nerves | 0.0342 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0083 |
| | 0.0377 | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 84

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0312 | 0.0153 | 2.0339 | 0.4917 |
| Breast | 0.0192 | 0.0320 | 0.6005 | 1.6654 |
| Small intestine | 0.0245 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0416 | 0.1439 | 6.9489 |
| Endocrine tissue | 0.0273 | 0.0451 | 0.6038 | 1.6562 |
| Gastrointestinal | 0.0230 | 0.0093 | 2.4850 | 0.4024 |
| Brain | 0.0177 | 0.0164 | 1.0799 | 0.9260 |
| Hematopoietic | 0.0174 | 0.0379 | 0.4587 | 2.1798 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0381 | 0.0065 | 5.8824 | 0.1700 |
| Heart | 0.0159 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0115 | 0.0351 | 0.3280 | 3.0489 |
| Lung | 0.0187 | 0.0123 | 1.5241 | 0.6561 |
| Stomach-esophagus | 0.0000 | 0.0460 | 0.0000 | undef |
| Muscle-skeleton | 0.0120 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0109 | 0.0205 | 0.5287 | 1.8915 |
| Pancreas | 0.0083 | 0.0166 | 0.4986 | 2.0057 |
| Penis | 0.0180 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0131 | 0.0064 | 2.0473 | 0.4885 |
| Uterus-endometrium | 0.0405 | 0.0528 | 0.7682 | 1.3018 |
| Uterus-myometrium | 0.0305 | 0.0204 | 1.4964 | 0.6683 |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0327 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0165 | | | |
| Cervix | 0.0000 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------------|---|
| Development | Breast 0.0272 |
| Gastrointestinal 0.0557 | Ovary_n 0.0000 |
| Brain 0.0222 | Ovary_t 0.0152 |
| Hematopoietic 0.0250 | Endocrine tissue 0.0000 |
| Skin 0.0118 | Fetal 0.0151 |
| Hepatic 0.0000 | Gastrointestinal 0.0000 |
| Heart-blood vessels 0.0000 | Hematopoietic 0.0259 |
| Lung 0.0249 | Skin-muscle 0.0000 |
| Suprarenal gland 0.0181 | Testicles 0.0246 |
| Kidney 0.0000 | Lung 0.0341 |
| Placenta 0.0062 | Nerves 0.0274 |
| Prostate 0.0242 | Prostate 0.0000 |
| Sensory organs 0.0249 | Sensory Organs 0.0125 |
| | Uterus_n |

Electronic Northern for SEQ. ID NO.: 85

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|----------------|-----|
| Bladder | 0.0000 | 0.0102 | 0.0000 undef | |
| Breast | 0.0051 | 0.0395 | 0.1296 7.7146 | |
| Small intestine | 0.0092 | 0.0165 | 0.5561 1.7982 | |
| Ovary | 0.0030 | 0.0312 | 0.0959 10.4234 | |
| Endocrine tissue | 0.0000 | 0.0050 | 0.0000 undef | |
| Gastrointestinal | 0.0038 | 0.0139 | 0.2761 3.6217 | |
| Brain | 0.0081 | 0.0113 | 0.7200 1.3890 | |
| Hematopoietic | 0.0027 | 0.0000 | undef 0.0000 | |
| Skin | 0.0000 | 0.0000 | undef undef | |
| Hepatic | 0.0000 | 0.0000 | undef undef | |
| Heart | 0.0074 | 0.0000 | undef 0.0000 | |
| Testicles | 0.0000 | 0.0117 | 0.0000 undef | |
| Lung | 0.0062 | 0.0020 | 3.0482 0.3281 | |
| Stomach-esophagus | 0.0097 | 0.0077 | 1.2605 0.7933 | |
| Muscle-skeleton | 0.0034 | 0.0120 | 0.2856 3.5020 | |
| Kidney | 0.0027 | 0.0000 | undef 0.0000 | |
| Pancreas | 0.0033 | 0.0000 | undef 0.0000 | |
| Penis | 0.0030 | 0.1066 | 0.0281 35.6140 | |
| Prostate | 0.0044 | 0.0043 | 1.0236 0.9769 | |
| Uterus-endometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-myometrium | 0.0076 | 0.0000 | undef 0.0000 | |
| Uterus-general | 0.0153 | 0.0000 | undef 0.0000 | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0030 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0026 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0039 | Fetal | 0.0087 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0333 |

Electronic Northern for SEQ. ID NO.: 88

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0195 | 0.0486 | 0.4014 | 2.4911 |
| Breast | 0.0064 | 0.0338 | 0.1890 | 5.2900 |
| Small intestine | 0.0153 | 0.0165 | 0.9268 | 1.0789 |
| Ovary | 0.0030 | 0.0182 | 0.1645 | 6.0803 |
| Endocrine tissue | 0.0136 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0134 | 0.0139 | 0.9664 | 1.0348 |
| Brain | 0.0052 | 0.0123 | 0.4200 | 2.3811 |
| Hematopoietic | 0.0361 | 0.0379 | 0.9528 | 1.0496 |
| Skin | 0.0184 | 0.0847 | 0.2166 | 4.6168 |
| Hepatic | 0.0048 | 0.0388 | 0.1225 | 8.1599 |
| Heart | 0.0074 | 0.0962 | 0.0771 | 12.9706 |
| Testicles | 0.0115 | 0.0234 | 0.4920 | 2.0326 |
| Lung | 0.0665 | 0.0573 | 1.1612 | 0.8612 |
| Stomach-esophagus | 0.0193 | 0.0383 | 0.5042 | 1.9833 |
| Muscle-skeleton | 0.0788 | 0.0300 | 2.6271 | 0.3807 |
| Kidney | 0.0027 | 0.0068 | 0.3965 | 2.5219 |
| Pancreas | 0.0116 | 0.0166 | 0.6980 | 1.4326 |
| Penis | 0.0000 | 0.0800 | 0.0000 | undef |
| Prostate | 0.0065 | 0.0106 | 0.6142 | 1.6282 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0954 | 0.0000 | undef |
| Uterus-general | 0.0128 | | | |
| Breast hyperplasia | 0.0089 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.1682 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0000 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0557 |
| Hematopoietic | Endocrine tissue 0.0000 |
| Skin | Fetal 0.0064 |
| Hepatic | Gastrointestinal 0.0122 |
| Heart-blood vessels | Hematopoietic 0.0057 |
| Lung | Skin-muscle 0.0032 |
| Suprarenal gland | Testicles 0.0000 |
| Kidney | Lung 0.0000 |
| Placenta | Nerves 0.0000 |
| Prostate | Prostate 0.0000 |
| Sensory organs | Sensory Organs 0.0125 |
| | Uterus_n |

Electronic Northern for SEQ. ID NO.: 89

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0128 | 0.3051 | 3.2777 |
| Breast | 0.0153 | 0.0038 | 4.0832 | 0.2449 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0208 | 0.0000 | undef |
| Endocrine tissue | 0.0068 | 0.0025 | 2.7170 | 0.3681 |
| Gastrointestinal | 0.0077 | 0.0046 | 1.6567 | 0.6036 |
| Brain | 0.0052 | 0.0021 | 2.5199 | 0.3968 |
| Hematopoietic | 0.0174 | 0.0000 | undef | 0.0000 |
| Skin | 0.0844 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0201 | 0.0275 | 0.7324 | 1.3653 |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef |
| Lung | 0.0156 | 0.0061 | 2.5402 | 0.3937 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0034 | 0.0060 | 0.5711 | 1.7510 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0050 | 0.0055 | 0.8974 | 1.1143 |
| Penis | 0.0329 | 0.1066 | 0.3089 | 3.2376 |
| Prostate | 0.0022 | 0.0021 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | 0.0000 | undef | undef |
| Prostate hyperplasia | 0.0030 | 0.0000 | undef | undef |
| Seminal vesicle | 0.0089 | 0.0000 | undef | undef |
| Sensory organs | 0.0118 | 0.0000 | undef | undef |
| White blood cells | 0.0121 | 0.0000 | undef | undef |
| Cervix | 0.0852 | 0.0000 | undef | undef |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0136 |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0063 | Endocrine tissue | 0.0000 |
| Skin | 0.0079 | Fetal | 0.0087 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0107 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0000 | Lung | 0.0164 |
| Placenta | 0.0000 | Nerves | 0.0020 |
| Prostate | 0.0061 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0125 |

Electronic Northern for SEQ. ID NO.: 90

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0117 | 0.0102 | 1.1441 | 0.8741 |
| Breast | 0.0038 | 0.0169 | 0.2268 | 4.4083 |
| Small intestine | 0.0184 | 0.0165 | 1.1122 | 0.8991 |
| Ovary | 0.0000 | 0.0182 | 0.0000 | undef |
| Endocrine tissue | 0.0051 | 0.0326 | 0.1567 | 6.3796 |
| Gastrointestinal | 0.0057 | 0.0093 | 0.6213 | 1.6096 |
| Brain | 0.0067 | 0.0062 | 1.0799 | 0.9260 |
| Hematopoietic | 0.0080 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0201 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0083 | 0.0143 | 0.5806 | 1.7223 |
| Stomach-esophagus | 0.0000 | 0.0153 | 0.0000 | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0109 | 0.0137 | 0.7930 | 1.2610 |
| Pancreas | 0.0033 | 0.0000 | undef | 0.0000 |
| Penis | 0.0120 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0128 | 0.5118 | 1.9538 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0356 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0052 | | | |
| Cervix | 0.0000 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0000 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0000 |
| Hematopoietic | Endocrine tissue 0.0000 |
| Skin | Fetal 0.0064 |
| Hepatic | Gastrointestinal 0.0000 |
| Heart-blood vessels | Hematopoietic 0.0057 |
| Lung | Skin-muscle 0.0130 |
| Suprarenal gland | Testicles 0.0231 |
| Kidney | Lung 0.0164 |
| Placenta | Nerves 0.0060 |
| Prostate | Prostate 0.0137 |
| Sensory organs | Sensory Organs 0.0000 |
| | Uterus_n 0.0042 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0078 | 0.0077 | 1.0170 | 0.9833 |
| Breast | 0.0051 | 0.0094 | 0.5444 | 1.8368 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0119 | 0.0150 | 0.7925 | 1.2619 |
| Gastrointestinal | 0.0057 | 0.0093 | 0.6213 | 1.6096 |
| Brain | 0.0081 | 0.0082 | 0.9899 | 1.0102 |
| Hematopoietic | 0.0120 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0127 | 0.0412 | 0.3084 | 3.2426 |
| Testicles | 0.0173 | 0.0000 | undef | 0.0000 |
| Lung | 0.0073 | 0.0307 | 0.2371 | 4.2179 |
| Lung | 0.0290 | 0.0383 | 0.7563 | 1.3222 |
| Stomach-esophagus | 0.0086 | 0.0060 | 1.4278 | 0.7004 |
| Muscle-skeleton | 0.0054 | 0.0274 | 0.1983 | 5.0439 |
| Kidney | 0.0033 | 0.0166 | 0.1994 | 5.0142 |
| Pancreas | 0.0150 | 0.0533 | 0.2808 | 3.5614 |
| Penis | 0.0000 | 0.0106 | 0.0000 | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-endometrium | 0.0051 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0064 | | | |
| Uterus-general | 0.0059 | | | |
| Breast hyperplasia | 0.0089 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0035 | | | |
| Sensory organs | 0.0106 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0064 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0071 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0130 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0328 |
| Placenta | 0.0121 | Nerves | 0.0040 |
| Prostate | 0.0000 | Prostate | 0.0274 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 92

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|----------------|-----|
| Bladder | 0.0000 | 0.0000 | undef undef | |
| Breast | 0.0038 | 0.0132 | 0.2917 3.4287 | |
| Small intestine | 0.0031 | 0.0165 | 0.1854 5.3946 | |
| Ovary | 0.0000 | 0.0182 | 0.0000 undef | |
| Endocrine tissue | 0.0051 | 0.0075 | 0.6792 1.4722 | |
| Gastrointestinal | 0.0038 | 0.0000 | undef 0.0000 | |
| Brain | 0.0015 | 0.0000 | undef 0.0000 | |
| Hematopoietic | 0.0000 | 0.0000 | undef undef | |
| Skin | 0.0073 | 0.0000 | undef 0.0000 | |
| Hepatic | 0.0048 | 0.0000 | undef 0.0000 | |
| Heart | 0.0011 | 0.0137 | 0.0771 12.9706 | |
| Testicles | 0.0000 | 0.0000 | undef undef | |
| Lung | 0.0145 | 0.0061 | 2.3708 0.4218 | |
| Stomach-esophagus | 0.0000 | 0.0153 | 0.0000 undef | |
| Muscle-skeleton | 0.0017 | 0.0000 | undef 0.0000 | |
| Kidney | 0.0054 | 0.0000 | undef 0.0000 | |
| Pancreas | 0.0017 | 0.0000 | undef 0.0000 | |
| Penis | 0.0030 | 0.0000 | undef 0.0000 | |
| Prostate | 0.0000 | 0.0000 | undef undef | |
| Uterus-endometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-myometrium | 0.0051 | 0.0000 | undef 0.0000 | |
| Uterus-general | 0.0032 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0235 | | | |
| Sensory organs | 0.0139 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0068 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0079 | Fetal | 0.0047 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0000 | Lung | 0.0164 |
| Placenta | 0.0061 | Nerves | 0.0040 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | | | | |
| Breast | 0.0000 | 0.0153 | 0.0000 | undef |
| Small intestine | 0.0077 | 0.0113 | 0.6805 | 1.4694 |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0030 | 0.0286 | 0.1047 | 9.5548 |
| Gastrointestinal | 0.0034 | 0.0075 | 0.4528 | 2.2083 |
| Brain | 0.0019 | 0.0093 | 0.2071 | 4.8289 |
| Hematopoietic | 0.0059 | 0.0082 | 0.7200 | 1.3890 |
| Skin | 0.0067 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0042 | 0.0000 | undef | 0.0000 |
| Lung | 0.0115 | 0.0234 | 0.4920 | 2.0326 |
| Stomach-esophagus | 0.0021 | 0.0061 | 0.3387 | 2.9526 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0051 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0054 | 0.0068 | 0.7930 | 1.2610 |
| Penis | 0.0017 | 0.0331 | 0.0499 | 20.0570 |
| Prostate | 0.0090 | 0.0267 | 0.3369 | 2.9678 |
| Uterus-endometrium | 0.0044 | 0.0021 | 2.0473 | 0.4885 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0051 | 0.0000 | undef | 0.0000 |
| Prostate hyperplasia | 0.0032 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0009 | | | |
| Cervix | 0.0000 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0063 | Endocrine tissue | 0.0245 |
| Skin | 0.0039 | Fetal | 0.0116 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0114 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0036 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0062 | Nerves | 0.0070 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0125 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0000 | 0.0051 | 0.0000 | undef |
| Breast | 0.0115 | 0.0132 | 0.8750 | 1.1429 |
| Small intestine | 0.0337 | 0.0496 | 0.6797 | 1.4713 |
| Ovary | 0.0030 | 0.0390 | 0.0768 | 13.0292 |
| Endocrine tissue | 0.0085 | 0.0251 | 0.3396 | 2.9444 |
| Gastrointestinal | 0.0747 | 0.0879 | 0.8501 | 1.1763 |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0194 | 0.2451 | 4.0800 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0351 | 0.0000 | undef |
| Lung | 0.0042 | 0.0143 | 0.2903 | 3.4446 |
| Stomach-esophagus | 0.0483 | 0.0077 | 6.3027 | 0.1587 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0163 | 0.0137 | 1.1896 | 0.8406 |
| Pancreas | 0.0231 | 0.0166 | 1.3960 | 0.7163 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0065 | 0.0106 | 0.6142 | 1.6282 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0064 | | | |
| Breast hyperplasia | 0.0119 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0083 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0188 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Fetal | 0.0035 |
| Heart-blood vessels | 0.0036 | Gastrointestinal | 0.0244 |
| Lung | 0.0108 | Hematopoietic | 0.0000 |
| Suprarenal gland | 0.0000 | Skin-muscle | 0.0000 |
| Kidney | 0.0124 | Testicles | 0.0000 |
| Placenta | 0.0000 | Lung | 0.0246 |
| Prostate | 0.0000 | Nerves | 0.0000 |
| Sensory organs | 0.0000 | Prostate | 0.0000 |
| | | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 95

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.1092 | 0.0460 | 2.3729 | 0.4214 |
| Breast | 0.0627 | 0.0865 | 0.7249 | 1.3795 |
| Small intestine | 0.1012 | 0.1158 | 0.8739 | 1.1443 |
| Ovary | 0.0599 | 0.1509 | 0.3970 | 2.5190 |
| Endocrine tissue | 0.0852 | 0.2984 | 0.2854 | 3.5039 |
| Gastrointestinal | 0.0900 | 0.0925 | 0.9733 | 1.0274 |
| Brain | 0.1811 | 0.0637 | 2.8450 | 0.3515 |
| Hematopoietic | 0.0521 | 0.1136 | 0.4587 | 2.1798 |
| Skin | 0.0587 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0809 | 0.0582 | 1.3889 | 0.7200 |
| Heart | 0.1092 | 0.0962 | 1.1344 | 0.8815 |
| Testicles | 0.0230 | 0.0234 | 0.9839 | 1.0163 |
| Lung | 0.0634 | 0.1104 | 0.5739 | 1.7425 |
| Stomach-esophagus | 0.0387 | 0.0460 | 0.8404 | 1.1900 |
| Muscle-skeleton | 0.0463 | 0.0420 | 1.1014 | 0.9079 |
| Kidney | 0.0706 | 0.1369 | 0.5155 | 1.9400 |
| Pancreas | 0.0743 | 0.1049 | 0.7085 | 1.4114 |
| Penis | 0.1467 | 0.0800 | 1.8345 | 0.5451 |
| Prostate | 0.0567 | 0.0873 | 0.6491 | 1.5405 |
| Uterus-endometrium | 0.0811 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.1067 | 0.1155 | 0.9242 | 1.0820 |
| Uterus-general | 0.0204 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.1407 | | | |
| Prostate hyperplasia | 0.0713 | | | |
| Seminal vesicle | 0.0534 | | | |
| Sensory organs | 0.0353 | | | |
| White blood cells | 0.0390 | | | |
| Cervix | 0.0532 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0068 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0253 |
| Hematopoietic | Endocrine tissue 0.0000 |
| Skin | Fetal 0.0116 |
| Hepatic | Gastrointestinal 0.0122 |
| Heart-blood vessels | Hematopoietic 0.0000 |
| Lung | Skin-muscle 0.0454 |
| Suprarenal gland | Testicles 0.0077 |
| Kidney | Lung 0.0246 |
| Placenta | Nerves 0.0753 |
| Prostate | Prostate 0.0205 |
| Sensory organs | Sensory Organs 0.0077 |
| | Uterus_n 0.0500 |

Electronic Northern for SEQ. ID NO.: 96

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0051 | 0.7627 | 1.3111 |
| Breast | 0.0013 | 0.0038 | 0.3403 | 2.9389 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0025 | 1.3585 | 0.7361 |
| Gastrointestinal | 0.0057 | 0.0093 | 0.6213 | 1.6096 |
| Brain | 0.0015 | 0.0041 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0061 | 0.1693 | 5.9051 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0136 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0017 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0079 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0010 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 97

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0117 | 0.0102 | 1.1441 | 0.8741 |
| Breast | 0.0077 | 0.0075 | 1.0208 | 0.9796 |
| Small intestine | 0.0061 | 0.0331 | 0.1854 | 5.3946 |
| Ovary | 0.0030 | 0.0390 | 0.0768 | 13.0292 |
| Endocrine tissue | 0.0051 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0019 | 0.0093 | 0.2071 | 4.8289 |
| Brain | 0.0044 | 0.0154 | 0.2880 | 3.4724 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0970 | 0.0980 | 10.1999 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0115 | 0.0000 | undef | 0.0000 |
| Lung | 0.0789 | 0.0532 | 1.4850 | 0.6734 |
| Stomach-esophagus | 0.0290 | 0.0077 | 3.7816 | 0.2644 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0027 | 0.0205 | 0.1322 | 7.5658 |
| Pancreas | 0.0033 | 0.0055 | 0.5983 | 1.6714 |
| Penis | 0.0120 | 0.0267 | 0.4493 | 2.2259 |
| Prostate | 0.0153 | 0.0021 | 7.1654 | 0.1396 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0445 | | | |
| Sensory organs | 0.1411 | | | |
| White blood cells | 0.0026 | | | |
| Cervix | 0.1917 | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0340 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0101 |
| Hematopoietic | Endocrine tissue 0.0000 |
| Skin | Fetal 0.0047 |
| Hepatic | Gastrointestinal 0.0000 |
| Heart-blood vessels | Hematopoietic 0.0057 |
| Lung | Skin-muscle 0.0000 |
| Suprarenal gland | Testicles 0.0000 |
| Kidney | Lung 0.0000 |
| Placenta | Nerves 0.0068 |
| Prostate | Prostate 0.0000 |
| Sensory organs | Sensory Organs 0.0000 |
| | Uterus_n 0.0000 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0000 | undef | undef |
| Breast | 0.0013 | 0.0056 | 0.2268 | 4.4083 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0130 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0093 | 0.0000 | undef |
| Brain | 0.0007 | 0.0021 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0095 | 0.0000 | undef | 0.0000 |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0234 | 0.0000 | undef |
| Lung | 0.0021 | 0.0020 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0017 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0735 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0010 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0083 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 99

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0039 | 0.0026 | 1.5254 | 0.6555 |
| Small intestine | 0.0090 | 0.0056 | 1.5879 | 0.6298 |
| Ovary | 0.0031 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0156 | 0.0000 | undef |
| Gastrointestinal | 0.0051 | 0.0025 | 2.0377 | 0.4907 |
| Brain | 0.0019 | 0.0046 | 0.4142 | 2.4145 |
| Hematopoietic | 0.0015 | 0.0041 | 0.3600 | 2.7779 |
| Skin | 0.0013 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0037 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0074 | 0.0000 | undef | 0.0000 |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0031 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0097 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0103 | 0.0060 | 1.7133 | 0.5837 |
| Pancreas | 0.0081 | 0.0068 | 1.1896 | 0.8406 |
| Penis | 0.0050 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0090 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0044 | 0.0064 | 0.6824 | 1.4654 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0204 |
| Brain | 0.0028 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0101 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0134 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0122 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0036 | Testicles | 0.0097 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0164 |
| Prostate | 0.0424 | Prostate | 0.0100 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0077 |
| | | | 0.0042 |

Electronic Northern for SEQ. ID NO.: 100

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0312 | 0.0179 | 1.7434 | 0.5736 |
| Breast | 0.0205 | 0.0244 | 0.8376 | 1.1939 |
| Small intestine | 0.0675 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0442 | 0.1354 | 7.3832 |
| Endocrine tissue | 0.0051 | 0.0025 | 2.0377 | 0.4907 |
| Gastrointestinal | 0.0862 | 0.0463 | 1.8638 | 0.5365 |
| Brain | 0.0067 | 0.0133 | 0.4984 | 2.0063 |
| Hematopoietic | 0.0120 | 0.0000 | undef | 0.0000 |
| Skin | 0.0477 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0143 | 0.0388 | 0.3676 | 2.7200 |
| Heart | 0.0212 | 0.0412 | 0.5140 | 1.9456 |
| Testicles | 0.0230 | 0.0234 | 0.9839 | 1.0163 |
| Lung | 0.0374 | 0.0450 | 0.8313 | 1.2029 |
| Stomach-esophagus | 0.0290 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0137 | 0.0600 | 0.2284 | 4.3775 |
| Kidney | 0.0054 | 0.0274 | 0.1983 | 5.0439 |
| Pancreas | 0.0066 | 0.0442 | 0.1496 | 6.6857 |
| Penis | 0.0449 | 0.0267 | 1.6847 | 0.5936 |
| Prostate | 0.0240 | 0.0234 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0136 | 1.6834 | 0.5940 |
| Uterus-general | 0.0255 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0384 | | | |
| Prostate hyperplasia | 0.0238 | | | |
| Seminal vesicle | 0.0534 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0303 | | | |
| Cervix | 0.0319 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | | Breast | |
| Gastrointestinal | 0.0278 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0304 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0064 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0122 |
| Lung | 0.0213 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0072 | Testicles | 0.0227 |
| Kidney | 0.0000 | Lung | 0.0309 |
| Placenta | 0.0000 | Nerves | 0.0164 |
| Prostate | 0.0182 | Prostate | 0.0020 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0137 |
| | | Uterus n | 0.0000 |
| | | | 0.0042 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0039 | 0.0077 | 0.5085 | 1.9666 |
| Small intestine | 0.0000 | 0.0188 | 0.0000 | undef |
| Ovary | 0.0245 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0120 | 0.0442 | 0.2709 | 3.6916 |
| Gastrointestinal | 0.0000 | 0.0025 | 0.0000 | undef |
| Brain | 0.0134 | 0.0185 | 0.7248 | 1.3797 |
| Hematopoietic | 0.0007 | 0.0072 | 0.1029 | 9.7228 |
| Skin | 0.0321 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0037 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0129 | 0.0000 | undef |
| Testicles | 0.0021 | 0.0000 | undef | 0.0000 |
| Lung | 0.0000 | 0.0234 | 0.0000 | undef |
| Stomach-esophagus | 0.0478 | 0.0450 | 1.0623 | 0.9414 |
| Muscle-skeleton | 0.0676 | 0.0690 | 0.9804 | 1.0200 |
| Kidney | 0.0069 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0068 | 0.0000 | undef |
| Penis | 0.0116 | 0.0055 | 2.0940 | 0.4775 |
| Prostate | 0.0030 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0065 | 0.0128 | 0.5118 | 1.9538 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0235 | | | |
| Sensory organs | 0.1101 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/ SUBTRACTED | |
|---------------------|-------------|--------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0139 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0039 | Fetal | 0.0029 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0366 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0036 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 102

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0234 | 0.0588 | 0.3979 | 2.5129 |
| Breast | 0.0179 | 0.0507 | 0.3529 | 2.8339 |
| Small intestine | 0.0245 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0180 | 0.0546 | 0.3289 | 3.0402 |
| Endocrine tissue | 0.0324 | 0.0251 | 1.2906 | 0.7749 |
| Gastrointestinal | 0.0364 | 0.0786 | 0.4629 | 2.1603 |
| Brain | 0.0067 | 0.0216 | 0.3086 | 3.2409 |
| Hematopoietic | 0.0174 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0323 | 0.1471 | 6.7999 |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0115 | 0.0117 | 0.9839 | 1.0163 |
| Lung | 0.0270 | 0.0225 | 1.2008 | 0.8328 |
| Stomach-esophagus | 0.0290 | 0.0383 | 0.7563 | 1.3222 |
| Muscle-skeleton | 0.0034 | 0.0060 | 0.5711 | 1.7510 |
| Kidney | 0.0326 | 0.0616 | 0.5287 | 1.8915 |
| Pancreas | 0.0132 | 0.0607 | 0.2176 | 4.5964 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0458 | 0.0617 | 0.7412 | 1.3491 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0152 | 0.0068 | 2.2445 | 0.4455 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0352 | | | |
| Prostate hyperplasia | 0.0476 | | | |
| Seminal vesicle | 0.0356 | | | |
| Sensory organs | 0.0353 | | | |
| White blood cells | 0.0069 | | | |
| Cervix | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|--------|-------------------------|--------|
| % frequency | | LIBRARIES | |
| | | % frequency | |
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0136 |
| Brain | 0.0167 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0125 | Ovary_t | 0.0253 |
| Skin | 0.0079 | Endocrine tissue | 0.0000 |
| Hepatic | 0.0000 | Fetal | 0.0169 |
| Heart-blood vessels | 0.0000 | Gastrointestinal | 0.0488 |
| Lung | 0.0325 | Hematopoietic | 0.0114 |
| Suprarenal gland | 0.0000 | Skin-muscle | 0.0000 |
| Kidney | 0.0124 | Testicles | 0.0231 |
| Placenta | 0.0303 | Lung | 0.0164 |
| Prostate | 0.0249 | Nerves | 0.0100 |
| Sensory organs | 0.0000 | Prostate | 0.0205 |
| | | Sensory Organs | 0.0077 |
| | | Uterus n | 0.0083 |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0351 | 0.0256 | 1.3729 | 0.7284 |
| Small intestine | 0.0077 | 0.0094 | 0.8166 | 1.2245 |
| Ovary | 0.0153 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0156 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0211 | 0.0463 | 0.4556 | 2.1950 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0027 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0110 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0065 | 0.0000 | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0125 | 0.0204 | 0.6096 | 1.6403 |
| Stomach-esophagus | 0.0290 | 0.0307 | 0.9454 | 1.0578 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0244 | 0.0068 | 3.5687 | 0.2802 |
| Pancreas | 0.0066 | 0.0110 | 0.5983 | 1.6714 |
| Penis | 0.0090 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0109 | 0.0170 | 0.6398 | 1.5631 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0954 | 0.0000 | undef |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0178 | | | |
| Seminal vesicle | 0.0178 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0000 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | 0.0272 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0056 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0010 |
| Placenta | 0.0242 | Nerves | 0.0137 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0312 | 0.0230 | 1.3559 | 0.7375 |
| Breast | 0.0435 | 0.0320 | 1.3611 | 0.7347 |
| Small intestine | 0.0429 | 0.0165 | 2.5952 | 0.3853 |
| Ovary | 0.0210 | 0.0676 | 0.3100 | 3.2263 |
| Endocrine tissue | 0.0341 | 0.0752 | 0.4528 | 2.2083 |
| Gastrointestinal | 0.0230 | 0.0185 | 1.2425 | 0.8048 |
| Brain | 0.0525 | 0.0554 | 0.9466 | 1.0564 |
| Hematopoietic | 0.0067 | 0.0000 | undef | 0.0000 |
| Skin | 0.0330 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0143 | 0.0259 | 0.5515 | 1.8133 |
| Heart | 0.0329 | 0.0962 | 0.3414 | 2.9288 |
| Testicles | 0.0115 | 0.0117 | 0.9839 | 1.0163 |
| Lung | 0.0166 | 0.0327 | 0.5080 | 1.9684 |
| Lung | 0.0193 | 0.0307 | 0.6303 | 1.5866 |
| Stomach-esophagus | 0.0343 | 0.0240 | 1.4278 | 0.7004 |
| Muscle-skeleton | 0.0624 | 0.0822 | 0.7600 | 1.3158 |
| Kidney | 0.0182 | 0.0055 | 3.2906 | 0.3039 |
| Pancreas | 0.0419 | 0.0000 | undef | 0.0000 |
| Penis | 0.0174 | 0.0405 | 0.4310 | 2.3202 |
| Prostate | 0.0135 | 0.1055 | 0.1280 | 7.8106 |
| Uterus-endometrium | 0.0381 | 0.0136 | 2.8057 | 0.3564 |
| Uterus-myometrium | 0.0662 | 0.0954 | 0.6939 | 1.4412 |
| Uterus-general | 0.0608 | | | |
| Uterus-general | 0.0476 | | | |
| Breast hyperplasia | 0.0623 | | | |
| Prostate hyperplasia | 0.0235 | | | |
| Seminal vesicle | 0.0035 | | | |
| Sensory organs | 0.0213 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0278 | Ovary_n | 0.0000 |
| Brain | 0.0500 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0876 | Endocrine tissue | 0.0490 |
| Skin | 0.0039 | Fetal | 0.0047 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0488 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0142 | Skin-muscle | 0.0356 |
| Suprarenal gland | 0.0434 | Testicles | 0.0154 |
| Kidney | 0.0000 | Lung | 0.0410 |
| Placenta | 0.0556 | Nerves | 0.0402 |
| Prostate | 0.0364 | Prostate | 0.0205 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | 0.1130 | Uterus n | 0.0375 |

Electronic Northern for SEQ. ID NO.: 106

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0195 | 0.0639 | 0.3051 | 3.2777 |
| Breast | 0.0333 | 0.0470 | 0.7077 | 1.4129 |
| Small intestine | 0.0399 | 0.1819 | 0.2191 | 4.5647 |
| Ovary | 0.0150 | 0.0702 | 0.2132 | 4.6905 |
| Endocrine tissue | 0.0238 | 0.0903 | 0.2642 | 3.7857 |
| Gastrointestinal | 0.0900 | 0.1110 | 0.8111 | 1.2329 |
| Brain | 0.0067 | 0.0267 | 0.2492 | 4.0126 |
| Hematopoietic | 0.0067 | 0.0000 | undef | 0.0000 |
| Skin | 0.0587 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0143 | 0.0323 | 0.4412 | 2.2666 |
| Heart | 0.0011 | 0.0962 | 0.0110 | 90.7941 |
| Testicles | 0.0000 | 0.0234 | 0.0000 | undef |
| Lung | 0.0062 | 0.0184 | 0.3387 | 2.9526 |
| Stomach-esophagus | 0.0483 | 0.3527 | 0.1370 | 7.2985 |
| Muscle-skeleton | 0.0000 | 0.0360 | 0.0000 | undef |
| Kidney | 0.0733 | 0.1575 | 0.4655 | 2.1483 |
| Pancreas | 0.0694 | 0.0276 | 2.5128 | 0.3980 |
| Penis | 0.0090 | 0.0533 | 0.1685 | 5.9357 |
| Prostate | 0.0109 | 0.0255 | 0.4265 | 2.3446 |
| Uterus-endometrium | 0.0270 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0272 | 0.2806 | 3.5642 |
| Uterus-general | 0.0000 | 0.4771 | 0.0000 | undef |
| Breast hyperplasia | 0.0576 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.1068 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0061 | | | |
| Cervix | 0.0319 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0111 | Ovary_n | 0.0000 |
| Brain | 0.0813 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0122 |
| Hepatic | 0.0000 | Gastrointestinal | 0.4149 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0145 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0309 | Lung | 0.0573 |
| Placenta | 0.0121 | Nerves | 0.0040 |
| Prostate | 0.0249 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 107

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0078 | 0.0204 | 0.3814 | 2.6222 |
| Small intestine | 0.0102 | 0.0132 | 0.7777 | 1.2858 |
| Ovary | 0.0153 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0208 | 0.0000 | undef |
| Gastrointestinal | 0.0119 | 0.0075 | 1.5849 | 0.6309 |
| Brain | 0.0307 | 0.0093 | 3.3134 | 0.3018 |
| Hematopoietic | 0.0111 | 0.0144 | 0.7714 | 1.2964 |
| Skin | 0.0094 | 0.0379 | 0.2470 | 4.0483 |
| Hepatic | 0.0441 | 0.0000 | undef | 0.0000 |
| Heart | 0.0095 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0170 | 0.0000 | undef | 0.0000 |
| Lung | 0.0058 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0229 | 0.0245 | 0.9314 | 1.0737 |
| Muscle-skeleton | 0.0097 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0034 | 0.0120 | 0.2856 | 3.5020 |
| Pancreas | 0.0190 | 0.0205 | 0.9252 | 1.0808 |
| Penis | 0.0083 | 0.0110 | 0.7479 | 1.3371 |
| Prostate | 0.0030 | 0.0267 | 0.1123 | 8.9035 |
| Uterus-endometrium | 0.0065 | 0.0106 | 0.6142 | 1.6282 |
| Uterus-myometrium | 0.0405 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0272 | 0.0000 | undef |
| Breast hyperplasia | 0.0000 | 0.0000 | undef | undef |
| Prostate hyperplasia | 0.0096 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0191 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|---------------------|----------------------|---|
| Development | | Breast |
| Gastrointestinal | 0.0278 | Ovary_n |
| Brain | 0.0083 | Ovary_t |
| Hematopoietic | 0.0188 | Endocrine tissue |
| Skin | 0.0079 | Fetal |
| Hepatic | 0.0000 | Gastrointestinal |
| Heart-blood vessels | 0.0107 | Hematopoietic |
| Lung | 0.0072 | Skin-muscle |
| Suprarenal gland | 0.0254 | Testicles |
| Kidney | 0.0185 | Lung |
| Placenta | 0.0000 | Nerves |
| Prostate | 0.0000 | Prostate |
| Sensory organs | 0.0000 | Sensory Organs |
| | | Uterus_n |

0.0068
0.0000
0.0000
0.0000
0.0041
0.0000
0.0000
0.0097
0.0000
0.0082
0.0131
0.0068
0.0000
0.0125

Electronic Northern for SEQ. ID NO.: 108

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|-----|
| Bladder | 0.0000 | 0.0051 | 0.0000 undef | |
| Breast | 0.0051 | 0.0132 | 0.3889 2.5715 | |
| Small intestine | 0.0061 | 0.0000 | undef 0.0000 | |
| Ovary | 0.0000 | 0.0156 | 0.0000 undef | |
| Endocrine tissue | 0.0034 | 0.0125 | 0.2717 3.6805 | |
| Gastrointestinal | 0.0077 | 0.0000 | undef 0.0000 | |
| Brain | 0.0037 | 0.0062 | 0.6000 1.6668 | |
| Hematopoietic | 0.0080 | 0.0000 | undef 0.0000 | |
| Skin | 0.0037 | 0.0000 | undef 0.0000 | |
| Hepatic | 0.0048 | 0.0129 | 0.3676 2.7200 | |
| Heart | 0.0032 | 0.0000 | undef 0.0000 | |
| Testicles | 0.0058 | 0.0000 | undef 0.0000 | |
| Lung | 0.0093 | 0.0123 | 0.7621 1.3122 | |
| Stomach-esophagus | 0.0097 | 0.0153 | 0.6303 1.5866 | |
| Muscle-skeleton | 0.0034 | 0.0000 | undef 0.0000 | |
| Kidney | 0.0027 | 0.0068 | 0.3965 2.5219 | |
| Pancreas | 0.0017 | 0.0055 | 0.2991 3.3428 | |
| Penis | 0.0090 | 0.0267 | 0.3369 2.9678 | |
| Prostate | 0.0392 | 0.0213 | 1.8425 0.5427 | |
| Uterus-endometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-myometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-general | 0.0051 | 0.0000 | undef 0.0000 | |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0238 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0104 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0056 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0105 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0285 |
| Lung | 0.0000 | Skin-muscle | 0.0324 |
| Suprarenal gland | 0.0072 | Testicles | 0.0077 |
| Kidney | 0.0000 | | 0.0246 |
| Placenta | 0.0247 | Lung | 0.0020 |
| Prostate | 0.0000 | Nerves | 0.0410 |
| Sensory organs | 0.0000 | Prostate | 0.0000 |
| | | Sensory Organs | 0.0167 |
| | | Uterus_n | |

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|---------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | | | | |
| Breast | 0.0078 | 0.0102 | 0.7627 | 1.3111 |
| Small intestine | 0.0166 | 0.0262 | 0.5898 | 1.6955 |
| Ovary | 0.0031 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0060 | 0.0390 | 0.1535 | 6.5146 |
| Gastrointestinal | 0.0392 | 0.0527 | 0.7439 | 1.3442 |
| Brain | 0.0153 | 0.0370 | 0.4142 | 2.4145 |
| Hematopoietic | 0.0059 | 0.0072 | 0.8228 | 1.2153 |
| Skin | 0.0080 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0110 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0129 | 0.0000 | undef |
| Testicles | 0.0064 | 0.0687 | 0.0925 | 10.8088 |
| Lung | 0.0058 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0239 | 0.0470 | 0.5080 | 1.9684 |
| Muscle-skeleton | 0.0000 | 0.0077 | 0.0000 | undef |
| Kidney | 0.0120 | 0.0120 | 0.9994 | 1.0006 |
| Pancreas | 0.0299 | 0.0000 | undef | 0.0000 |
| Penis | 0.0182 | 0.0110 | 1.6453 | 0.6078 |
| Prostate | 0.0210 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0305 | 0.0106 | 2.8662 | 0.3489 |
| Uterus-myometrium | 0.0203 | 0.1055 | 0.1920 | 5.2070 |
| Uterus-general | 0.0076 | 0.0136 | 0.5611 | 1.7821 |
| Breast hyperplasia | 0.0102 | 0.0000 | undef | 0.0000 |
| Prostate hyperplasia | 0.0352 | | | |
| Seminal vesicle | 0.0446 | | | |
| Sensory organs | 0.0267 | | | |
| White blood cells | 0.0353 | | | |
| Cervix | 0.0147 | | | |
| | 0.0106 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0068 |
| Brain | 0.0222 | Ovary_t | 0.1595 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0101 |
| Skin | 0.0197 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0408 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0366 |
| Lung | 0.0178 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0145 | Testicles | 0.0259 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0185 | Nerves | 0.0410 |
| Prostate | 0.0000 | Prostate | 0.0151 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0342 |
| | 0.0126 | Uterus n | 0.0155 |
| | | | 0.0125 |

Electronic Northern for SEQ. ID NO.: 111

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | | | | |
| Breast | 0.0117 | 0.0460 | 0.2542 | 3.9333 |
| Small intestine | 0.0192 | 0.0376 | 0.5104 | 1.9593 |
| Ovary | 0.0000 | 0.0496 | 0.0000 | undef |
| Endocrine tissue | 0.0030 | 0.0234 | 0.1279 | 7.8175 |
| Gastrointestinal | 0.0017 | 0.0000 | undef | 0.0000 |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0007 | 0.0000 | undef | 0.0000 |
| Skin | 0.0013 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0147 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0065 | 0.0000 | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0058 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0062 | 0.0102 | 0.6096 | 1.6403 |
| Muscle-skeleton | 0.0193 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0271 | 0.0137 | 1.9826 | 0.5044 |
| Penis | 0.0132 | 0.0221 | 0.5983 | 1.6714 |
| Prostate | 0.0030 | 0.0267 | 0.1123 | 8.9035 |
| Uterus-endometrium | 0.0240 | 0.0298 | 0.8043 | 1.2434 |
| Uterus-myometrium | 0.0000 | 0.0528 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0352 | 0.0954 | 0.0000 | undef |
| Prostate hyperplasia | 0.0149 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0106 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|---------------------|----------------------|---|
| Development | | Breast |
| Gastrointestinal | 0.0000 | Ovary_n |
| Brain | 0.0000 | Ovary_t |
| Hematopoietic | 0.0000 | Endocrine tissue |
| Skin | 0.0000 | Fetal |
| Hepatic | 0.0000 | Gastrointestinal |
| Heart-blood vessels | 0.0000 | Hematopoietic |
| Lung | 0.0000 | Skin-muscle |
| Suprarenal gland | 0.0000 | Testicles |
| Kidney | 0.0000 | Lung |
| Placenta | 0.0000 | Nerves |
| Prostate | 0.0000 | Prostate |
| Sensory organs | 0.0000 | Sensory Organs |
| | | Uterus_n |

Electronic Northern for SEQ. ID NO.: 112

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0039 | 0.0051 | 0.7627 | 1.3111 |
| Breast | 0.0051 | 0.0207 | 0.2475 | 4.0410 |
| Small intestine | 0.0123 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0338 | 0.0886 | 11.2920 |
| Endocrine tissue | 0.0017 | 0.0025 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0038 | 0.0185 | 0.2071 | 4.8289 |
| Brain | 0.0022 | 0.0092 | 0.2400 | 4.1669 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0847 | 0.0433 | 23.0839 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0053 | 0.0275 | 0.1927 | 5.1882 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0042 | 0.0041 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0109 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0033 | 0.0055 | 0.5983 | 1.6714 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0044 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0051 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0178 | | | |
| Seminal vesicle | 0.0118 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0213 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0354 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0079 | Fetal | 0.0035 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0114 |
| Lung | 0.0071 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0036 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0020 |
| Placenta | 0.0062 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0155 |
| Sensory organs | 0.0249 | Sensory Organs | 0.0375 |
| | 0.0251 | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 113

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0117 | 0.0409 | 0.2860 | 3.4963 |
| Breast | 0.0256 | 0.0376 | 0.6805 | 1.4694 |
| Small intestine | 0.0399 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0390 | 0.2303 | 4.3431 |
| Endocrine tissue | 0.0477 | 0.0702 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0479 | 0.0231 | 2.0708 | 0.4829 |
| Brain | 0.0229 | 0.0349 | 0.6564 | 1.5234 |
| Hematopoietic | 0.0281 | 0.0000 | undef | 0.0000 |
| Skin | 0.0624 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0259 | 0.1838 | 5.4400 |
| Heart | 0.0519 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0230 | 0.0468 | 0.4920 | 2.0326 |
| Lung | 0.0270 | 0.0491 | 0.5504 | 1.8170 |
| Stomach-esophagus | 0.0387 | 0.0230 | 1.6807 | 0.5950 |
| Muscle-skeleton | 0.0377 | 0.0840 | 0.4487 | 2.2286 |
| Kidney | 0.0462 | 0.0411 | 1.1235 | 0.8901 |
| Pancreas | 0.0116 | 0.0276 | 0.4188 | 2.3877 |
| Penis | 0.0150 | 0.0533 | 0.2808 | 3.5614 |
| Prostate | 0.0283 | 0.0490 | 0.5786 | 1.7284 |
| Uterus-endometrium | 0.0541 | 0.0528 | 1.0243 | 0.9763 |
| Uterus-myometrium | 0.0305 | 0.0272 | 1.1223 | 0.8911 |
| Uterus-general | 0.0255 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0192 | | | |
| Prostate hyperplasia | 0.0386 | | | |
| Seminal vesicle | 0.0267 | | | |
| Sensory organs | 0.0353 | | | |
| White blood cells | 0.0312 | | | |
| Cervix | 0.0213 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0611 | Ovary_n | 0.1595 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0157 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0029 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0320 | Hematopoietic | 0.0000 |
| Lung | 0.0397 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0507 | Testicles | 0.0164 |
| Kidney | 0.0247 | Lung | 0.0050 |
| Placenta | 0.0303 | Nerves | 0.0068 |
| Prostate | 0.1247 | Prostate | 0.0000 |
| Sensory organs | 0.0377 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 115

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0051 | 0.7627 | 1.3111 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0702 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0192 | 0.0185 | 1.0354 | 0.9658 |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0058 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0052 | 0.0020 | 2.5402 | 0.3937 |
| Lung | 0.0193 | 0.0230 | 0.8404 | 1.1900 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0017 | 0.0110 | 0.1496 | 6.6857 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0065 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0954 | 0.0000 | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0118 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0047 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0114 |
| Lung | 0.0000 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0010 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0167 |
| | | Uterus_n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0000 | 0.0026 | 0.0000 | undef |
| Breast | 0.0038 | 0.0038 | 1.0208 | 0.9796 |
| Small intestine | 0.0061 | 0.0165 | 0.3707 | 2.6973 |
| Ovary | 0.0030 | 0.0208 | 0.1439 | 6.9489 |
| Endocrine tissue | 0.0102 | 0.0025 | 4.0755 | 0.2454 |
| Gastrointestinal | 0.0057 | 0.0046 | 1.2425 | 0.8048 |
| Brain | 0.0030 | 0.0031 | 0.9599 | 1.0417 |
| Hematopoietic | 0.0094 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0095 | 0.0000 | undef | 0.0000 |
| Heart | 0.0058 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0073 | 0.0123 | 0.5927 | 1.6872 |
| Lung | 0.0000 | 0.0077 | 0.0000 | undef |
| Stomach-esophagus | 0.0051 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0081 | 0.0068 | 1.1896 | 0.8406 |
| Kidney | 0.0017 | 0.0055 | 0.2991 | 3.3428 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0065 | 0.0021 | 3.0709 | 0.3256 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0064 | | | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0078 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0035 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0032 |
| Lung | 0.0036 | Skin-muscle | 0.0154 |
| Suprarenal gland | 0.0254 | Testicles | 0.0082 |
| Kidney | 0.0124 | Lung | 0.0060 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0208 |
| | | Uterus n | |

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|---------|
| Bladder | 0.0078 | 0.0128 | 0.6102 | 1.6399 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0208 | 0.0000 | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0517 | 0.0879 | 0.5886 | 1.6991 |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0381 | 0.0518 | 0.7353 | 1.3600 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0010 | 0.0164 | 0.0635 | 15.7470 |
| Lung | 0.0290 | 0.0230 | 1.2605 | 0.7933 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0033 | 0.0110 | 0.2991 | 3.3428 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0022 | 0.0043 | 0.5118 | 1.9538 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0051 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | | undef | 0.0000 |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | | | | |
| White blood cells | | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0051 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | | Sensory Organs | 0.0000 |
| | | Uterus n | 0.0000 |

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0000 | 0.0026 | 0.0000 | undef |
| Breast | 0.0013 | 0.0056 | 0.2268 | 4.4083 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0019 | 0.0046 | 0.4142 | 2.4145 |
| Brain | 0.0022 | 0.0031 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0010 | 0.0061 | 0.1693 | 5.9051 |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0068 | 0.3965 | 2.5219 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0021 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0030 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0114 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0249 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0155 |
| | | Uterus n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 121

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0117 | 0.0153 | 0.7627 | 1.3111 |
| Breast | 0.0026 | 0.0132 | 0.1944 | 5.1431 |
| Small intestine | 0.0031 | 0.0165 | 0.1854 | 5.3946 |
| Ovary | 0.0000 | 0.0156 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0019 | 0.0046 | 0.4142 | 2.4145 |
| Brain | 0.0030 | 0.0062 | 0.4800 | 2.0835 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.1760 | 0.0518 | 3.4008 | 0.2941 |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0117 | 0.4920 | 2.0326 |
| Lung | 0.0010 | 0.0082 | 0.1270 | 7.8735 |
| Lung | 0.0000 | 0.0077 | 0.0000 | undef |
| Stomach-esophagus | 0.0188 | 0.0060 | 3.1411 | 0.3184 |
| Muscle-skeleton | 0.0081 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0033 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0174 | 0.0277 | 0.6299 | 1.5875 |
| Prostate | 0.0000 | 0.0528 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0954 | 0.0000 | undef |
| Uterus-general | 0.0032 | | | |
| Breast hyperplasia | 0.0119 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0235 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency |
|----------------------|---|
| Development | Breast 0.0000 |
| Gastrointestinal | Ovary_n 0.0000 |
| Brain | Ovary_t 0.0203 |
| Hematopoietic | Endocrine tissue 0.0000 |
| Skin | Fetal 0.0035 |
| Hepatic | Gastrointestinal 0.0000 |
| Heart-blood vessels | Hematopoietic 0.0000 |
| Lung | Skin-muscle 0.0000 |
| Suprarenal gland | Testicles 0.0000 |
| Kidney | Lung 0.0010 |
| Placenta | Nerves 0.0000 |
| Prostate | Prostate 0.0000 |
| Sensory organs | Sensory Organs 0.0000 |
| | Uterus_n |

Electronic Northern for SEQ. ID NO.: 122

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.1053 | 0.1125 | 0.9361 | 1.0683 |
| Breast | 0.1164 | 0.1015 | 1.1468 | 0.8720 |
| Small intestine | 0.0491 | 0.0662 | 0.7415 | 1.3487 |
| Ovary | 0.0479 | 0.1015 | 0.4723 | 2.1173 |
| Endocrine tissue | 0.0562 | 0.0251 | 2.2415 | 0.4461 |
| Gastrointestinal | 0.1015 | 0.1758 | 0.5777 | 1.7311 |
| Brain | 0.0296 | 0.1273 | 0.2322 | 4.3058 |
| Hematopoietic | 0.0535 | 0.0000 | undef | 0.0000 |
| Skin | 0.2166 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0809 | 0.1035 | 0.7813 | 1.2800 |
| Heart | 0.4133 | 0.2612 | 1.5825 | 0.6319 |
| Testicles | 0.0748 | 0.0468 | 1.5989 | 0.6254 |
| Lung | 0.1506 | 0.1227 | 1.2278 | 0.8145 |
| Stomach-esophagus | 0.2126 | 0.1073 | 1.9808 | 0.5048 |
| Muscle-skeleton | 0.0805 | 0.1680 | 0.4793 | 2.0863 |
| Kidney | 0.0543 | 0.0890 | 0.6100 | 1.6393 |
| Pancreas | 0.0562 | 0.1712 | 0.3281 | 3.0479 |
| Penis | 0.1497 | 0.2399 | 0.6240 | 1.6026 |
| Prostate | 0.0850 | 0.0362 | 2.3483 | 0.4258 |
| Uterus-endometrium | 0.0541 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0457 | 0.1019 | 0.4489 | 2.2276 |
| Uterus-general | 0.0560 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0991 | | | |
| Prostate hyperplasia | 0.0832 | | | |
| Seminal vesicle | 0.0801 | | | |
| Sensory organs | 0.1059 | | | |
| White blood cells | 0.0720 | | | |
| Cervix | 0.0639 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0835 | Breast | 0.0544 |
| Gastrointestinal | 0.0361 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0433 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0466 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0610 |
| Heart-blood vessels | 0.0961 | Hematopoietic | 0.0000 |
| Lung | 0.0867 | Skin-muscle | 0.0421 |
| Suprarenal gland | 0.0761 | Testicles | 0.0000 |
| Kidney | 0.0309 | Lung | 0.1474 |
| Placenta | 0.1151 | Nerves | 0.0110 |
| Prostate | 0.5984 | Prostate | 0.0205 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 123

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0039 | 0.0026 | 1.5254 | 0.6555 |
| Breast | 0.0013 | 0.0019 | 0.6805 | 1.4694 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0182 | 0.0000 | undef |
| Endocrine tissue | 0.0017 | 0.0075 | 0.2264 | 4.4166 |
| Gastrointestinal | 0.0000 | 0.0093 | 0.0000 | undef |
| Brain | 0.0030 | 0.0021 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0053 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0115 | 0.0000 | undef | 0.0000 |
| Lung | 0.0010 | 0.0061 | 0.1693 | 5.9051 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0086 | 0.0060 | 1.4278 | 0.7004 |
| Kidney | 0.0027 | 0.0205 | 0.1322 | 7.5658 |
| Pancreas | 0.0066 | 0.0055 | 1.1966 | 0.8357 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0021 | 2.0473 | 0.4885 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|---|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0134 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0130 |
| Lung | 0.0254 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0062 | Testicles | 0.0164 |
| Kidney | 0.0182 | Lung | 0.0030 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | | Sensory Organs | 0.0125 |
| | | Uterus_n | |

Electronic Northern for Seq. ID: 258

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N | |
|-------------------|-------------------|------------------|-------------------|--------|
| B lymphoma | | | | |
| Bladder | 0.0025 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0047 | 0.0000 | undef |
| Large intestine | 0.0018 | 0.0014 | 1.2524 | 0.7985 |
| Small intestine | 0.0019 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0027 | 0.0213 | 0.1288 | 7.7625 |
| Endocrine tissue | 0.0000 | 0.0167 | 0.0000 | undef |
| Brain | 0.0064 | 0.0000 | undef | 0.0000 |
| Skin | 0.0012 | 0.0010 | 1.1605 | 0.8617 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0051 | 0.0000 | undef | 0.0000 |
| Lung | 0.0080 | 0.0118 | 0.6786 | 1.4737 |
| Stomach-esophagus | 0.0029 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0037 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0017 | 0.0000 | undef | 0.0000 |
| T lymphoma | 0.0019 | 0.0000 | undef | 0.0000 |
| Uterus | 0.0025 | 0.0000 | undef | 0.0000 |
| White blood cells | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0040 | | | |
| Penis | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0139 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0036 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0035 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0194 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0098 |
| Lungs_t | 0.0000 |
| Nerves | 0.0030 |
| Kidney t | 0.0000 |
| Ovary uterus | 0.0000 |
| Prostate n | 0.0121 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

000127 04231900

Electronic Northern for Seq. ID: 259

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | | | |
| Bladder | | | |
| Breast | 0.0000 | 0.0000 | undef undef |
| Large intestine | 0.0117 | 0.0023 | 4.9785 0.2009 |
| Small intestine | 0.0070 | 0.0014 | 5.0097 0.1996 |
| Ovary | 0.0000 | 0.0057 | 0.0000 undef |
| Endocrine tissue | 0.0082 | 0.0000 | undef 0.0000 |
| Brain | 0.0000 | 0.0119 | 0.0000 undef |
| Skin | 0.0032 | 0.0089 | 0.3621 2.7613 |
| Hepatic | 0.0006 | 0.0000 | undef 0.0000 |
| Heart | 0.0037 | 0.0000 | undef 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef undef |
| Lung | 0.0081 | 0.0000 | undef 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef |
| Muscle-skeleton | 0.0019 | 0.0000 | undef 0.0000 |
| Kidney | 0.0145 | 0.0000 | undef 0.0000 |
| Pancreas | 0.0000 | 0.0037 | 0.0000 undef |
| Prostate | 0.0022 | 0.0000 | undef 0.0000 |
| T lymphoma | 0.0017 | 0.0000 | undef 0.0000 |
| Uterus | 0.0019 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0025 | 0.0075 | 0.3381 2.9576 |
| Hematopoietic | 0.0059 | 0.0138 | 0.4284 2.3344 |
| Penis | 0.0000 | 0.0000 | undef undef |
| Seminal vesicle | 0.0027 | | |
| Sensory organs | 0.0080 | | |
| | 0.0141 | | |
| | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0071 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0062 |
| Placenta | 0.0061 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0245 |
| Fetal | 0.0070 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0065 |
| Testicles_n | 0.0084 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0195 |
| Lungs_t | 0.0000 |
| Nerves | 0.0000 |
| Kidney t | 0.0000 |
| Ovary uterus | 0.0061 |
| Prostate n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 260

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | | | |
| Bladder | 0.0000 | 0.0000 | undef undef |
| Breast | 0.0000 | 0.0023 | 0.0000 undef |
| Large intestine | 0.0062 | 0.0000 | undef 0.0000 |
| Small intestine | 0.0019 | 0.0085 | 0.2243 4.4591 |
| Ovary | 0.0000 | 0.0000 | undef undef |
| Endocrine tissue | 0.0000 | 0.0525 | 0.0000 undef |
| Brain | 0.0032 | 0.0071 | 0.4527 2.2091 |
| Skin | 0.0023 | 0.0020 | 1.1605 0.8617 |
| Hepatic | 0.0000 | 0.0000 | undef undef |
| Heart | 0.0000 | 0.0063 | 0.0000 undef |
| Testicles | 0.0051 | 0.0000 | undef 0.0000 |
| Lung | 0.0000 | 0.0000 | undef undef |
| Stomach-esophagus | 0.0088 | 0.0037 | 2.3680 0.4223 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef |
| Kidney | 0.0017 | 0.0000 | undef 0.0000 |
| Pancreas | 0.0022 | 0.0000 | undef 0.0000 |
| Prostate | 0.0083 | 0.0000 | undef 0.0000 |
| T lymphoma | 0.0028 | 0.0013 | 2.1706 0.4607 |
| Uterus | 0.0051 | 0.0224 | 0.2254 4.4364 |
| White blood cells | 0.0015 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0027 | 0.0304 | 0.0902 11.0896 |
| Penis | 0.0013 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0070 | | |
| | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0139 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0107 |
| Adrenal gland | 0.0036 |
| Kidney | 0.0000 |
| Placenta | 0.0062 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |
| | 0.0251 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0098 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0065 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0060 |
| Kidney t | 0.0000 |
| Ovary uterus | 0.0113 |
| Prostate n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | | | |
| Bladder | | | |
| Breast | 0.0025 | 0.0000 | undef 0.0000 |
| Large intestine | 0.0000 | 0.0000 | undef undef |
| Small intestine | 0.0009 | 0.0014 | 0.6262 1.5969 |
| Ovary | 0.0000 | 0.0000 | undef undef |
| Endocrine tissue | 0.0027 | 0.0000 | undef 0.0000 |
| Brain | 0.0000 | 0.0191 | 0.0000 undef |
| Skin | 0.0000 | 0.0000 | undef undef |
| Hepatic | 0.0006 | 0.0000 | undef 0.0000 |
| Heart | 0.0000 | 0.0000 | undef undef |
| Testicles | 0.0000 | 0.0000 | undef undef |
| Lung | 0.0010 | 0.0000 | undef 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef |
| Kidney | 0.0000 | 0.0000 | undef undef |
| Pancreas | 0.0000 | 0.0000 | undef undef |
| Prostate | 0.0000 | 0.0055 | 0.0000 undef |
| T lymphoma | 0.0019 | 0.0000 | undef 0.0000 |
| Uterus | 0.0051 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0015 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0034 | 0.0000 | undef 0.0000 |
| Penis | 0.0013 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0070 | | |
| | 0.0000 | | |

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0188 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0023 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0000 |
| Kidney t | 0.0023 |
| Ovary uterus | 0.0061 |
| Prostate_n | 0.0000 |
| Sensory Organs | 0.0000 |
| White blood cells | |

Electronic Northern for Seq. ID: 262

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0150 | 0.0000 | undef 0.0000 |
| Bladder | 0.0156 | 0.0023 | 6.6380 0.1506 |
| Breast | 0.0158 | 0.0056 | 2.8179 0.3549 |
| Large intestine | 0.0038 | 0.0028 | 1.3456 0.7432 |
| Small intestine | 0.0110 | 0.0320 | 0.3435 2.9109 |
| Ovary | 0.0178 | 0.0334 | 0.5333 1.8752 |
| Endocrine tissue | 0.0064 | 0.0213 | 0.3018 3.3136 |
| Brain | 0.0081 | 0.0060 | 1.3539 0.7386 |
| Skin | 0.0110 | 0.0000 | undef 0.0000 |
| Hepatic | 0.0139 | 0.0190 | 0.7324 1.3653 |
| Heart | 0.0193 | 0.0000 | undef 0.0000 |
| Testicles | 0.0080 | 0.0118 | 0.6786 1.4737 |
| Lung | 0.0175 | 0.0129 | 1.3531 0.7390 |
| Stomach-esophagus | 0.0000 | 0.0064 | 0.0000 undef |
| Muscle-skeleton | 0.0017 | 0.0111 | 0.1546 6.4671 |
| Kidney | 0.0045 | 0.0096 | 0.4642 2.1540 |
| Pancreas | 0.0132 | 0.0000 | undef 0.0000 |
| Prostate | 0.0104 | 0.0091 | 1.1370 0.8795 |
| T lymphoma | 0.0101 | 0.0149 | 0.6762 1.4788 |
| Uterus | 0.0192 | 0.0230 | 0.8353 1.1971 |
| White blood cells | 0.0055 | 0.0304 | 0.1803 5.5448 |
| Hematopoietic | 0.0067 | | |
| Penis | 0.0080 | | |
| Seminal vesicle | 0.0070 | | |
| Sensory organs | 0.0118 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0056 |
| Brain | 0.0000 |
| Hematopoietic | 0.0275 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0142 |
| Lung | 0.0000 |
| Adrenal gland | 0.0254 |
| Kidney | 0.0124 |
| Placenta | 0.0121 |
| Prostate | 0.0000 |
| Sensory organs | 0.0251 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0203 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0162 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0454 |
| Testicles_n | 0.0125 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0100 |
| Kidney t | 0.0000 |
| Ovary Uterus | 0.0293 |
| Prostate n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 263

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | | | |
| Bladder | 0.0125 | 0.0136 | 0.9198 1.0872 |
| Breast | 0.0039 | 0.0188 | 0.2075 4.8204 |
| Large intestine | 0.0114 | 0.0281 | 0.4070 2.4568 |
| Small intestine | 0.0211 | 0.0142 | 1.4801 0.6756 |
| Ovary | 0.0082 | 0.0000 | undef 0.0000 |
| Endocrine tissue | 0.0089 | 0.0286 | 0.3111 3.2147 |
| Brain | 0.0161 | 0.0151 | 1.0599 0.9435 |
| Skin | 0.0211 | 0.0110 | 1.9234 0.5199 |
| Hepatic | 0.0110 | 0.0000 | undef 0.0000 |
| Heart | 0.0046 | 0.0127 | 0.3662 2.7307 |
| Testicles | 0.0162 | 0.0000 | undef 0.0000 |
| Lung | 0.0080 | 0.0178 | 0.4523 2.2108 |
| Stomach-esophagus | 0.0136 | 0.0111 | 1.2278 0.8145 |
| Muscle-skeleton | 0.0072 | 0.0128 | 0.5666 1.7648 |
| Kidney | 0.0158 | 0.0185 | 1.0206 0.9799 |
| Pancreas | 0.0157 | 0.0145 | 1.0831 0.9232 |
| Prostate | 0.0083 | 0.0221 | 0.3739 2.6743 |
| T lymphoma | 0.0123 | 0.0039 | 3.1352 0.3190 |
| Uterus | 0.0000 | 0.0149 | 0.0000 undef |
| White blood cells | 0.0077 | 0.0230 | 0.3368 2.9694 |
| Hematopoietic | 0.0082 | 0.0000 | undef 0.0000 |
| Penis | 0.0094 | | |
| Seminal vesicle | 0.0107 | | |
| Sensory organs | 0.0070 | | |
| | 0.0235 | | |

FETUS % freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0111 |
| Brain | 0.0000 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0260 |
| Heart-blood vessels | 0.0107 |
| Lung | 0.0072 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0124 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.1595 |
| Ovary_t | 0.0203 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0069 |
| Gastrointestinal | 0.0488 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0032 |
| Testicles_n | 0.0167 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0195 |
| Lungs_t | 0.0000 |
| Nerves | 0.0060 |
| Kidney t | 0.0000 |
| Ovary uterus | 0.0158 |
| Prostate n | 0.0061 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N | |
|-------------------|-------------------|------------------|-------------------|--------|
| B lymphoma | | | | |
| Bladder | | | | |
| Breast | 0.0150 | 0.0136 | 1.1037 | 0.9060 |
| Large intestine | 0.0273 | 0.0211 | 1.2907 | 0.7748 |
| Small intestine | 0.0229 | 0.0632 | 0.3618 | 2.7639 |
| Ovary | 0.0268 | 0.0256 | 1.0466 | 0.9555 |
| Endocrine tissue | 0.0192 | 0.0000 | undef | 0.0000 |
| Brain | 0.0089 | 0.0501 | 0.1778 | 5.6255 |
| Skin | 0.0193 | 0.0142 | 1.3580 | 0.7364 |
| Hepatic | 0.0041 | 0.0160 | 0.2539 | 3.9391 |
| Heart | 0.0073 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0465 | 0.0254 | 1.8311 | 0.5461 |
| Lung | 0.0091 | 0.0412 | 0.2215 | 4.5144 |
| Stomach-esophagus | 0.0120 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0204 | 0.0185 | 1.1050 | 0.9049 |
| Kidney | 0.0290 | 0.0384 | 0.7557 | 1.3233 |
| Pancreas | 0.0069 | 0.0185 | 0.3711 | 2.6946 |
| Prostate | 0.0537 | 0.0289 | 1.8570 | 0.5385 |
| T lymphoma | 0.0380 | 0.0110 | 3.4403 | 0.2907 |
| Uterus | 0.0330 | 0.0130 | 2.5323 | 0.3949 |
| White blood cells | 0.0051 | 0.0075 | 0.6762 | 1.4788 |
| Hematopoietic | 0.0148 | 0.0138 | 1.0709 | 0.9338 |
| Penis | 0.0075 | 0.0000 | undef | 0.0000 |
| Seminal vesicle | 0.0147 | | | |
| Sensory organs | 0.0054 | | | |
| | 0.0000 | | | |
| | 0.0235 | | | |

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

| | |
|-------------------|--------|
| Breast | 0.0204 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary n | 0.0000 |
| Ovary_t | 0.0101 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0017 |
| Gastrointestinal | 0.0244 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs n | 0.0000 |
| Lungs_t | 0.0040 |
| Nerves | 0.0000 |
| Kidney t | 0.0090 |
| Ovary Uterus | 0.0121 |
| Prostate n | 0.0000 |
| Sensory Organs | 0.0000 |
| White blood cells | |

NORMAL
% freq.

TUMOR
% freq.

RATIOS
N/T T/N

| | 0.0000 | 0.0272 | 0.0000 undef |
|-------------------|--------|--------|---------------|
| B lymphoma | 0.0117 | 0.0023 | 4.9785 0.2009 |
| Bladder | 0.0141 | 0.0155 | 0.9109 1.0979 |
| Breast | 0.0920 | 0.0968 | 0.9498 1.0528 |
| Large intestine | 0.0247 | 0.0000 | undef 0.0000 |
| Small intestine | 0.0208 | 0.0882 | 0.2354 4.2478 |
| Ovary | 0.0016 | 0.0000 | undef 0.0000 |
| Endocrine tissue | 0.0000 | 0.0010 | 0.0000 undef |
| Brain | 0.0000 | 0.0000 | undef undef |
| Skin | 0.0000 | 0.0444 | 0.0000 undef |
| Hepatic | 0.0000 | 0.0000 | undef undef |
| Heart | 0.0000 | 0.0000 | undef undef |
| Testicles | 0.0000 | 0.0000 | undef undef |
| Lung | 0.0000 | 0.0000 | undef undef |
| Stomach-esophagus | 0.0165 | 0.0111 | 1.4909 0.6707 |
| Muscle-skeleton | 0.0362 | 0.0128 | 2.8338 0.3529 |
| Kidney | 0.0000 | 0.0000 | undef undef |
| Pancreas | 0.0000 | 0.0000 | undef undef |
| Prostate | 0.0000 | 0.0166 | 0.0000 undef |
| T lymphoma | 0.0207 | 0.0352 | 0.5895 1.6963 |
| Uterus | 0.0025 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0030 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef undef |
| Penis | 0.0027 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0915 | | |
| | 0.0118 | | |

FETUS
& freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0278 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0108 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES & frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0253 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0023 |
| Gastrointestinal | 0.0244 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0084 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0293 |
| Lungs_t | 0.0000 |
| Nerves | 0.0000 |
| Kidney t | 0.0000 |
| Ovary uterus | 0.0113 |
| Prostate n | 0.0182 |
| Sensory Organs | 0.0000 |
| White blood cells | 0.0000 |

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N | |
|-------------------|-------------------|------------------|-------------------|--------|
| B lymphoma | | | | |
| Bladder | 0.0025 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Large intestine | 0.0114 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0055 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0059 | 0.0525 | 0.1131 | 8.8401 |
| Brain | 0.0161 | 0.0035 | 4.5268 | 0.2209 |
| Skin | 0.0017 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0073 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0071 | 0.0000 | undef | 0.0000 |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0049 | 0.0037 | 1.3155 | 0.7601 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0470 | 0.0048 | 9.7491 | 0.1026 |
| Pancreas | 0.0033 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0019 | 0.0000 | undef | 0.0000 |
| T lymphoma | 0.0000 | 0.0000 | undef | undef |
| Uterus | 0.0044 | 0.0046 | 0.9638 | 1.0375 |
| White blood cells | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | | | |
| Penis | 0.0080 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0000 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

| | |
|-------------------|--------|
| Breast | 0.0068 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0000 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0020 |
| Nerves | 0.0000 |
| Kidney t | 0.0023 |
| Ovary uterus | 0.0000 |
| Prostate n | 0.0000 |
| Sensory Organs | 0.0000 |
| White blood cells | |

seq. 1
NORMAL
% freq.

TUMOR
% freq.

RATIOS
N/T T/N

| | % freq. | tumor % freq. | RATIO N/T T |
|-------------------|---------|---------------|---------------|
| B lymphoma | | | |
| Bladder | | | |
| Breast | 0.0050 | 0.0000 | undef 0.0000 |
| Large intestine | 0.0000 | 0.0070 | 0.0000 undef |
| Small intestine | 0.0026 | 0.0014 | 1.8786 0.5323 |
| Ovary | 0.0000 | 0.0000 | undef undef |
| Endocrine tissue | 0.0055 | 0.0000 | undef 0.0000 |
| Brain | 0.0000 | 0.0119 | 0.0000 undef |
| Skin | 0.0000 | 0.0000 | 0.0000 undef |
| Hepatic | 0.0029 | 0.0010 | 2.9013 0.3447 |
| Heart | 0.0000 | 0.0394 | 0.0000 undef |
| Testicles | 0.0000 | 0.0000 | undef undef |
| Lung | 0.0030 | 0.0000 | undef 0.0000 |
| Stomach-esophagus | 0.0040 | 0.0000 | undef 0.0000 |
| Muscle-skeleton | 0.0049 | 0.0000 | undef 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef undef |
| Pancreas | 0.0034 | 0.0000 | undef 0.0000 |
| Prostate | 0.0000 | 0.0048 | 0.0000 undef |
| T lymphoma | 0.0000 | 0.0000 | undef undef |
| Uterus | 0.0028 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0000 | 0.0000 | undef undef |
| Hematopoietic | 0.0000 | 0.0000 | undef undef |
| Penis | 0.0007 | 0.0000 | undef 0.0000 |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0054 | | |
| | 0.0000 | | |
| | 0.0000 | | |

FETUS
% freq.

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | |
| Breast_t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0035 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0042 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0010 |
| Kidney_t | 0.0000 |
| Ovary_uterus | 0.0023 |
| Prostate_n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N | |
|-------------------|-------------------|------------------|-------------------|--------|
| B lymphoma | | | | |
| Bladder | 0.0025 | 0.0000 | undef | 0.0000 |
| Breast | 0.0117 | 0.0094 | 1.2446 | 0.8035 |
| Large intestine | 0.0088 | 0.0253 | 0.3479 | 2.8744 |
| Small intestine | 0.0192 | 0.0028 | 6.7278 | 0.1486 |
| Ovary | 0.0192 | 0.0213 | 0.9018 | 1.1089 |
| Endocrine tissue | 0.0030 | 0.0143 | 0.2074 | 4.8219 |
| Brain | 0.0193 | 0.0035 | 5.4321 | 0.1841 |
| Skin | 0.0081 | 0.0249 | 0.3249 | 3.0774 |
| Hepatic | 0.0184 | 0.0000 | undef | 0.0000 |
| Heart | 0.0093 | 0.0063 | 1.4649 | 0.6826 |
| Testicles | 0.0112 | 0.0000 | undef | 0.0000 |
| Lung | 0.0040 | 0.0118 | 0.3393 | 2.9475 |
| Stomach-esophagus | 0.0126 | 0.0037 | 3.4204 | 0.2924 |
| Muscle-skeleton | 0.0072 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0120 | 0.0037 | 3.2472 | 0.3080 |
| Pancreas | 0.0157 | 0.0048 | 3.2497 | 0.3077 |
| Prostate | 0.0050 | 0.0110 | 0.4487 | 2.2285 |
| T lymphoma | 0.0104 | 0.0052 | 1.9897 | 0.5026 |
| Uterus | 0.0051 | 0.0000 | undef | 0.0000 |
| White blood cells | 0.0163 | 0.0092 | 1.7670 | 0.5659 |
| Hematopoietic | 0.0110 | 0.0000 | undef | 0.0000 |
| Penis | 0.0027 | | | |
| Seminal vesicle | 0.0054 | | | |
| Sensory organs | 0.0000 | | | |
| | 0.0000 | | | |

| | |
|---------------------|--------|
| Development | 0.0139 |
| Gastrointestinal | 0.0056 |
| Brain | 0.0063 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0036 |
| Lung | 0.0036 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0124 |
| Placenta | 0.0121 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast_t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0051 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0023 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0257 |
| Skin-muscle | 0.0032 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0010 |
| Nerves | 0.0000 |
| Kidney_t | 0.0023 |
| Ovary Uterus | 0.0243 |
| Prostate_n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | |

Electronic Northern for Seq. ID: 269

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | | | |
| Bladder | 0.0025 | 0.0000 | undef 0.0000 |
| Breast | 0.0156 | 0.0047 | 3.3190 0.3013 |
| Large intestine | 0.0079 | 0.0014 | 5.6359 0.1774 |
| Small intestine | 0.0096 | 0.0057 | 1.6820 0.5945 |
| Ovary | 0.0000 | 0.0000 | undef undef |
| Endocrine tissue | 0.0030 | 0.0191 | 0.1555 6.4291 |
| Brain | 0.0064 | 0.0018 | 3.6214 0.2761 |
| Skin | 0.0058 | 0.0060 | 0.9671 1.0340 |
| Hepatic | 0.0037 | 0.0000 | undef 0.0000 |
| Heart | 0.0000 | 0.0127 | 0.0000 undef |
| Testicles | 0.0091 | 0.0000 | undef 0.0000 |
| Lung | 0.0080 | 0.0000 | undef 0.0000 |
| Stomach-esophagus | 0.0068 | 0.0037 | 1.8417 0.5430 |
| Muscle-skeleton | 0.0000 | 0.0064 | 0.0000 undef |
| Kidney | 0.0034 | 0.0111 | 0.3093 3.2335 |
| Pancreas | 0.0045 | 0.0000 | undef 0.0000 |
| Prostate | 0.0083 | 0.0110 | 0.7479 1.3371 |
| T lymphoma | 0.0057 | 0.0117 | 0.4823 2.0732 |
| Uterus | 0.0025 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0044 | 0.0092 | 0.4819 2.0750 |
| Hematopoietic | 0.0034 | 0.0000 | undef 0.0000 |
| Penis | 0.0027 | | |
| Seminal vesicle | 0.0188 | | |
| Sensory organs | 0.0141 | | |
| | 0.0118 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0028 |
| Brain | 0.0000 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0107 |
| Lung | 0.0036 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0061 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large Intestine t | 0.0000 |
| Ovary n | 0.0000 |
| Ovary t | 0.0152 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0006 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0032 |
| Skin-muscle | 0.0000 |
| Testicles n | 0.0000 |
| Testicles t | 0.0000 |
| Lungs n | 0.0000 |
| Lungs t | 0.0020 |
| Nerves | 0.0000 |
| Kidney t | 0.0068 |
| Ovary uterus | 0.0000 |
| Prostate n | 0.0077 |
| Sensory organs | 0.0000 |
| White blood cells | |

NORMAL
% freq.

TUMOR
% freq.

RATIOS
N/T T/N

| | % freq. | % freq. | N/1 |
|-------------------|---------|---------|---------------|
| B lymphoma | | | |
| Bladder | 0.0075 | 0.0000 | undef 0.0000 |
| Breast | 0.0156 | 0.0047 | 3.3190 0.3013 |
| Large intestine | 0.0167 | 0.0197 | 0.8499 1.1767 |
| Small intestine | 0.0307 | 0.0199 | 1.5378 0.6503 |
| Ovary | 0.0082 | 0.0213 | 0.3865 2.5875 |
| Endocrine tissue | 0.0059 | 0.0334 | 0.1778 5.6255 |
| Brain | 0.0321 | 0.0248 | 1.2934 0.7732 |
| Skin | 0.0365 | 0.0170 | 2.1504 0.4650 |
| Hepatic | 0.0257 | 0.0000 | undef 0.0000 |
| Heart | 0.0000 | 0.0127 | 0.0000 undef |
| Testicles | 0.0426 | 0.0000 | undef 0.0000 |
| Lung | 0.0161 | 0.0118 | 1.3571 0.7369 |
| Stomach-esophagus | 0.0272 | 0.0222 | 1.2278 0.8144 |
| Muscle-skeleton | 0.0072 | 0.0000 | undef 0.0000 |
| Kidney | 0.0137 | 0.0074 | 1.8555 0.5389 |
| Pancreas | 0.0246 | 0.0145 | 1.7022 0.5875 |
| Prostate | 0.0050 | 0.0000 | undef 0.0000 |
| T lymphoma | 0.0179 | 0.0065 | 2.7494 0.3637 |
| Uterus | 0.0177 | 0.0672 | 0.2630 3.8026 |
| White blood cells | 0.0118 | 0.0046 | 2.5703 0.3891 |
| Hematopoietic | 0.0219 | 0.0000 | undef 0.0000 |
| Penis | 0.0147 | | |
| Seminal vesicle | 0.0188 | | |
| Sensory organs | 0.0281 | | |
| | 0.0000 | | |

FETUS
& freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0167 |
| Brain | 0.0188 |
| Hematopoietic | 0.0079 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0356 |
| Lung | 0.0108 |
| Adrenal gland | 0.0254 |
| Kidney | 0.0124 |
| Placenta | 0.0182 |
| Prostate | 0.0249 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0068 |
| Breast_t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.1595 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0110 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0227 |
| Testicles_n | 0.0125 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0195 |
| Lungs_t | 0.0000 |
| Nerves | 0.0281 |
| Kidney_t | 0.0000 |
| Ovary_uterus | 0.0068 |
| Prostate_n | 0.0061 |
| Prostate_t | 0.0232 |
| Sensory organs | 0.0000 |
| White blood cells | |

Electronic Northern for Seq. ID: 271

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | | | |
| Bladder | 0.0125 | 0.0407 | 0.3066 3.2617 |
| Breast | 0.0117 | 0.0164 | 0.7112 1.4061 |
| Large intestine | 0.0123 | 0.0098 | 1.2524 0.7985 |
| Small intestine | 0.0057 | 0.0057 | 1.0092 0.9909 |
| Ovary | 0.0165 | 0.0000 | undef 0.0000 |
| Endocrine tissue | 0.0030 | 0.0143 | 0.2074 4.8219 |
| Brain | 0.0096 | 0.0195 | 0.4938 2.0250 |
| Skin | 0.0122 | 0.0070 | 1.7408 0.5745 |
| Hepatic | 0.0110 | 0.0000 | undef 0.0000 |
| Heart | 0.0093 | 0.0000 | undef 0.0000 |
| Testicles | 0.0071 | 0.0137 | 0.5169 1.9347 |
| Lung | 0.0201 | 0.0059 | 3.3928 0.2947 |
| Stomach-esophagus | 0.0117 | 0.0148 | 0.7893 1.2669 |
| Muscle-skeleton | 0.0072 | 0.0320 | 0.2267 4.4110 |
| Kidney | 0.0086 | 0.0000 | undef 0.0000 |
| Pancreas | 0.0045 | 0.0096 | 0.4642 2.1540 |
| Prostate | 0.0017 | 0.0055 | 0.2992 3.3427 |
| T lymphoma | 0.0066 | 0.0117 | 0.5627 1.7770 |
| Uterus | 0.0126 | 0.0149 | 0.8453 1.1830 |
| White blood cells | 0.0059 | 0.0322 | 0.1836 5.4469 |
| Hematopoietic | 0.0062 | 0.0304 | 0.2029 4.9287 |
| Penis | 0.0107 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0141 | | |
| | 0.0235 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0111 |
| Brain | 0.0250 |
| Hematopoietic | 0.0118 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0071 |
| Lung | 0.0036 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0124 |
| Placenta | 0.0061 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0152 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0220 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0421 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0211 |
| Nerves | 0.0000 |
| Kidney t | 0.0248 |
| Ovary Uterus | 0.0000 |
| Prostate n | 0.0232 |
| Sensory organs | 0.0000 |
| White blood cells | |

NORMAL
% freq.

RATIOS
N/T T/N

FETUS
& freq.

STANDARDIZED/SUBTRACTED LIBRARIES & frequency

| | |
|-------------------|--------|
| Breast | 0.0136 |
| Breast t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0052 |
| Gastrointestinal | 0.0244 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0195 |
| Lungs_t | 0.0000 |
| Nerves | 0.0121 |
| Kidney t | 0.0000 |
| Ovary Uterus | 0.0000 |
| Prostate n | 0.0061 |
| Sensory Organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 273

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | | | |
| Bladder | 0.0025 | 0.0000 | undef 0.0000 |
| Breast | 0.0078 | 0.0188 | 0.4149 2.4104 |
| Large intestine | 0.0079 | 0.0112 | 0.7045 1.4195 |
| Small intestine | 0.0019 | 0.0057 | 0.3364 2.9727 |
| Ovary | 0.0055 | 0.0000 | undef 0.0000 |
| Endocrine tissue | 0.0030 | 0.0215 | 0.1383 7.2328 |
| Brain | 0.0080 | 0.0053 | 1.5089 0.6627 |
| Skin | 0.0041 | 0.0070 | 0.5803 1.7234 |
| Hepatic | 0.0147 | 0.0000 | undef 0.0000 |
| Heart | 0.0046 | 0.0000 | undef 0.0000 |
| Testicles | 0.0203 | 0.0000 | undef 0.0000 |
| Lung | 0.0000 | 0.0355 | 0.0000 undef |
| Stomach-esophagus | 0.0039 | 0.0111 | 0.3508 2.8506 |
| Muscle-skeleton | 0.0145 | 0.0128 | 1.1335 0.8822 |
| Kidney | 0.0120 | 0.0074 | 1.6236 0.6159 |
| Pancreas | 0.0000 | 0.0048 | 0.0000 undef |
| Prostate | 0.0000 | 0.0276 | 0.0000 undef |
| T lymphoma | 0.0085 | 0.0065 | 1.3023 0.7679 |
| Uterus | 0.0303 | 0.0149 | 2.0287 0.4929 |
| White blood cells | 0.0133 | 0.0092 | 1.4458 0.6917 |
| Hematopoietic | 0.0205 | 0.0000 | undef 0.0000 |
| Penis | 0.0027 | | |
| Seminal vesicle | 0.0054 | | |
| Sensory organs | 0.0000 | | |
| | 0.0118 | | |

FETUS % freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0028 |
| Brain | 0.0063 |
| Hematopoietic | 0.0118 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0213 |
| Lung | 0.0145 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0124 |
| Placenta | 0.0061 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

| | |
|-------------------|--------|
| Breast | 0.0068 |
| Breast_t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0152 |
| Fetal | 0.0245 |
| Gastrointestinal | 0.0023 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0065 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0098 |
| Nerves | 0.0000 |
| Kidney_t | 0.0060 |
| Ovary Uterus | 0.0000 |
| Prostate_n | 0.0090 |
| Sensory Organs | 0.0000 |
| White blood cells | 0.0000 |

2.2. Fisher Test

In order to decide whether a partial sequence *S* of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to *S*. If the null hypothesis can be rejected with high enough certainty, the gene belonging to *S* is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence *S* is completed in three steps:

1. Determination of all sequences homologous to *S* from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence *C* from the assembled sequences.

The consensus sequence *C* will generally be longer than initial sequence *S*. Its electronic Northern Blot will

accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i : iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from ovarian tumor tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute
(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones that contain the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well." In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

Seq. ID No.

Identified BACs

| | | | | | |
|-----|----------|----------|----------|----------|----------|
| 4 | 195/N/3 | 206/P/3 | 384/I/3 | 323/G/9 | |
| 5 | 222/B/10 | 404/E/10 | 526/F/20 | 565/P/11 | 279/F/14 |
| 9 | 501/L/21 | | | | |
| 11 | 490/P/4 | 321/I/23 | 410/F/5 | 443/N/20 | |
| 19 | 311/A/19 | 505/F/17 | 216/D/8 | 219/C/22 | |
| 29 | 382/N/10 | 539/L/7 | | | |
| 31 | 530/D/11 | | | | |
| 35 | 503/N/10 | | | | |
| 37 | 547/D/16 | 215/P/16 | 439/K/6 | | |
| 39 | 216/L/9 | 512/F/5 | 203/J/15 | | |
| 45 | 205/K/7 | 250/H/22 | 283/C/17 | 528/B/20 | 402/L/11 |
| 80 | 371/A/20 | 470/L/3 | 495/L/3 | | |
| 92 | 254/M/9 | 376/O/12 | 421/L/18 | 429/J/19 | |
| 112 | 243/O/14 | 520/K/15 | 565/J/17 | 565/J/24 | |

TABLE I

Col. 1 - Seq. ID No.
Col. 2 - Expression
Col. 3 - Function
Col. 4 - Modules
Col. 5 - Cytogenetic localization
Col. 6 - Nearest marker

TABLE I

| Seq. ID No. | Expression | Function |
|-------------------|---------------------------------------|----------|
| 1 | Overexpressed in ovarian tumor tissue | Unknown |
| 2 | Overexpressed in ovarian tumor tissue | Unknown |
| 3 | Overexpressed in ovarian tumor tissue | Unknown |
| 4 | Overexpressed in ovarian tumor tissue | P52r1PK |
| 5 | Overexpressed in ovarian tumor tissue | Unknown |
| 6 | Overexpressed in ovarian tumor tissue | Unknown |
| 7 | Overexpressed in ovarian tumor tissue | Unknown |
| 5 | Overexpressed in ovarian tumor tissue | Unknown |
| 5 | Overexpressed in ovarian tumor tissue | Unknown |
| 10 | Overexpressed in ovarian tumor tissue | Unknown |
| 12 | Overexpressed in ovarian tumor tissue | Unknown |
| 13 | Overexpressed in ovarian tumor tissue | Unknown |
| 15 | Overexpressed in ovarian tumor tissue | Unknown |
| 16 | Overexpressed in ovarian tumor tissue | Unknown |
| 18 | Overexpressed in ovarian tumor tissue | Unknown |
| 19 | Overexpressed in ovarian tumor tissue | Unknown |

TABELLE I

| Seq ID No. | Expression | Funktion | Module | Cytogenetische Lokalisation | nearest marker |
|------------|-----------------------------------|-----------|----------------|-----------------------------|---|
| 1 | in Ovariumorgewebe überexprimiert | unbekannt | | 1p31.1-p34.1 | SHGC-2542,2540,2456; D1S448-D1S500;; WI-6555; D1S198-D1S462 |
| 2 | in Ovariumorgewebe überexprimiert | unbekannt | | 2p22.3-p23.3 | SGC32173; D2S174-D2S390;; TIGR-A006H24;D2S392-D2S390 |
| 3 | in Ovariumorgewebe überexprimiert | unbekannt | | 4p15.1 | WI-15951 (D4S1043-SHGC-16179) |
| 4 | in Ovariumorgewebe überexprimiert | P52RIPK | | 11q13.5 - q14.1 | SHGC-31396 (SHGC-32287, D11S4681) |
| 5 | in Ovariumorgewebe überexprimiert | unbekannt | | 1q22 | SHGC-31641 |
| 6 | in Ovariumorgewebe überexprimiert | unbekannt | | 13q33.1 - q34 | AFM310yd5 |
| 7 | in Ovariumorgewebe überexprimiert | unbekannt | | 8q11.23-q12.1 | SHGC-32002; D8S1828-D8S507 |
| 8 | in Ovariumorgewebe überexprimiert | unbekannt | | 4q24 | SHGC-36699 |
| 9 | in Ovariumorgewebe überexprimiert | unbekannt | PRO_RICH | 2q35 | SHGH-32531 (D2S1297, SHGC-35278) |
| 10 | in Ovariumorgewebe überexprimiert | unbekannt | PHD | | |
| 12 | in Ovariumorgewebe überexprimiert | unbekannt | | 5q23.3-q31.1 | AFM200ya9=D5S414 |
| 13 | in Ovariumorgewebe überexprimiert | unbekannt | | 3p23 | WI-6841;D3S1599-D3S1583 |
| 15 | in Ovariumorgewebe überexprimiert | unbekannt | | 6q22.1-q24.3 | SHGC-33316; D6S453-D6S311 |
| 16 | in Ovariumorgewebe überexprimiert | unbekannt | NLS_BP | 10p15.3 | CDa1hh03; D10S533-D10S594;; SHGC-11812; D10S558-D10S591 |
| 18 | in Ovariumorgewebe überexprimiert | unbekannt | Ribosomal_L24e | 15q21.3-q22.1 | Cda17g12; D15S209-D15S198 |
| 19 | in Ovariumorgewebe überexprimiert | unbekannt | | 11q14.3 | SHGC-36010 (D11S1979, D11S1887) |

| Seq. ID No. | Expression | Function |
|-------------|---------------------------------------|--|
| 20 | Overexpressed in ovarian tumor tissue | Unknown |
| 21 | Overexpressed in ovarian tumor tissue | Unknown |
| 22 | Overexpressed in ovarian tumor tissue | Unknown |
| 23 | Overexpressed in ovarian tumor tissue | Unknown |
| 24 | Overexpressed in ovarian tumor tissue | Unknown |
| 25 | Overexpressed in ovarian tumor tissue | Branchio-oto-renal syndrome candidate gene |
| 26 | Overexpressed in ovarian tumor tissue | Unknown |
| 27 | Overexpressed in ovarian tumor tissue | Unknown |
| 28 | Overexpressed in ovarian tumor tissue | Unknown |
| 29 | Overexpressed in ovarian tumor tissue | Unknown |
| 30 | Overexpressed in ovarian tumor tissue | Unknown |
| 31 | Overexpressed in ovarian tumor tissue | Unknown |
| 32 | Overexpressed in ovarian tumor tissue | Partially homologous to R. norvegicus calpain |
| 33 | Overexpressed in ovarian tumor tissue | Partially homologous to human mRNA for fungal sterol-C5-desaturase homolog |
| 34 | Overexpressed in ovarian tumor tissue | Partially homologous to human GPx-3 mRNA for plasma glutathione peroxidase |
| 35 | Overexpressed in ovarian tumor tissue | Partially homologous to homo sapiens CHD2 mRNA |

| Seq ID No. | Expression | Funktion | Module | Cytogenetische Lokalisation | nearest marker |
|------------|-----------------------------------|--|----------|-----------------------------|---|
| 20 | in Ovartumorgewebe überexprimiert | unbekannt | | 3q22.2-3q22.3 | SHGC-34629 (SHGC-30855, SGC32794) |
| 21 | in Ovartumorgewebe überexprimiert | unbekannt | | 3q26.33-q29 | AFM308y1 (D3S2363, D3S3669) |
| 22 | in Ovartumorgewebe überexprimiert | unbekannt | | 7q11.23 | SHGC-37054 |
| 23 | in Ovartumorgewebe überexprimiert | unbekannt | | | |
| 24 | in Ovartumorgewebe überexprimiert | unbekannt | | 4q28.1-q31.1 | WI-30941; SGC30941; D4S1580-D4S427 |
| 25 | in Ovartumorgewebe überexprimiert | Branchio-oto-renal syndrome candidate gene | | 7q32.3-q33 | AFMc024we9 |
| 26 | in Ovartumorgewebe überexprimiert | unbekannt | NLS_BP | 17q23.3 | SHGC-64257 |
| 27 | in Ovartumorgewebe überexprimiert | unbekannt | | 17p12-p13.2 | SHGC-31370 (SHGC-35547-SHGC-35513) |
| 28 | in Ovartumorgewebe überexprimiert | unbekannt | | 10q22.3 | Cda0wf11, TIGR-A001X23; D10S607-D10S201 |
| 29 | in Ovartumorgewebe überexprimiert | unbekannt | | 11q13.2-q13.5 | WI-14303; D11S4136-D11S1314.; TIGR-A005U01; D11S913-D11S1314/RH; SHGC-14407 |
| 30 | in Ovartumorgewebe überexprimiert | unbekannt | | 7p21.3 | SHGC-14339 |
| 31 | in Ovartumorgewebe überexprimiert | unbekannt | | 12p12.3 | AFMb320va9 |
| 32 | in Ovartumorgewebe überexprimiert | Partielles Homolog zu R. norvegicus calpain | | 1q41 | SHGC-3992 (D1S2550-D1S2568) |
| 33 | in Ovartumorgewebe überexprimiert | Partiell Homolog zu Human mRNA for fungal sterol-C5-desaturase homolog | Thymosin | 11q23.3 | WI-19895; D11S924-D11S925 |
| 34 | in Ovartumorgewebe überexprimiert | Partiell homolog zu Human GPx-3 mRNA for plasma glutathione peroxidase | GSHPx | 5q33.1 | SHGC-10972 |
| 35 | in Ovartumorgewebe überexprimiert | Partiell Homolog zu Homo sapiens CHD2 mRNA | | 19q13.13-q13.2 | AFMb018wh1 |

| Seq. ID No. | Expression | Function |
|-------------|---------------------------------------|---|
| 36 | Overexpressed in ovarian tumor tissue | Human homolog to M. musculus formin binding protein 21 |
| 38 | Overexpressed in ovarian tumor tissue | Human homolog to Tribolium castaneum zinc finger protein |
| 39 | Overexpressed in ovarian tumor tissue | Human homolog to S. cerevisiae chromosome II sequence for ORF YBR1725 |
| 40 | Overexpressed in ovarian tumor tissue | Human homolog to Rattus norvegicus rsly 1p |
| 41 | Overexpressed in ovarian tumor tissue | Human homolog to PEC-60=gastrointestinal peptide, swine |
| 42 | Overexpressed in ovarian tumor tissue | Human homolog to Mus musculus mCAF1 protein |
| 43 | Overexpressed in ovarian tumor tissue | Human homolog to Mouse mitochondrial genome; unidentified reading frame |
| 44 | Overexpressed in ovarian tumor tissue | Human homolog to Mouse kidney androgen-regulated protein (KAP) |
| 45 | Overexpressed in ovarian tumor tissue | Human homolog to M. musculus Tera |
| 46 | Overexpressed in ovarian tumor tissue | Human homolog to Caenorhabditis elegans cosmid T27F7 |
| 47 | Overexpressed in ovarian tumor tissue | Human homolog to Caenorhabditis elegans cosmid T27F7 |
| 48 | Overexpressed in ovarian tumor tissue | Human homolog to Caenorhabditis elegans cosmid K11H12 |
| 49 | Overexpressed in ovarian tumor tissue | Human homolog to Caenorhabditis elegans cosmid C43E11 |

| Seq ID No. | Expression | Funktion | Module | Cytogenetische Lokalisation | nearest marker |
|------------|-----------------------------------|---|-------------------|-------------------------------|--------------------------------------|
| 36 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu M. musculus formin binding protein 21 | WW_rsp5_WWP | | |
| 38 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Tribolium castaneum zinc finger protein | | 2p13.1-p16.1;RH: 2p13.1-p13.3 | siSG31094; D2S292-D2S145 |
| 39 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu S. cerevisiae chromosome II sequence for ORF YBR1725 | | 19q12 | AFM205y10 (D19S1080, D19S590) |
| 40 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Rattus norvegicus rsly1p | Sec1 | 17 | |
| 41 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu PEC-60=gastrointestinal peptide, swine | kazal | | |
| 42 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Mus musculus mCAF1 protein | | 8p22-p23.3 | BDA16f11; D8S549-D8S1733 bzw. S280 |
| 43 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Mouse mitochondrial genome; Unidentified reading frame | oxidoreduced_q1_N | | |
| 44 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Mouse kidney androgen-regulated protein (KAP) | | 1p36.31-p36.13 | SHGC-11461 (D1S2565, SGC32561) |
| 45 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu M. musculus Tera | | 12p11.21-p11.23 | SHGC-1349 (D1S1621/D1S1805) |
| 46 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Caenorhabditis elegans cosmid T27F7 | | 19q13.33-qter | SHGC-30173; D19S418-qTEL |
| 47 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Caenorhabditis elegans cosmid T27F7 | PRO_RICH | 2p11.1-p11.2 | D2S388-D2S2181 |
| 48 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Caenorhabditis elegans cosmid K11H12 | UPF0005 | 10q23.1 | SHGC-167+SHGC-11466; D10S551-D10S532 |
| 49 | in Ovariumorgewebe überexprimiert | Humanes Homolog zu Caenorhabditis elegans cosmid C43E11 | PRO_RICH | Xq22.3-Xq25 | siSG2963; DXS1059-DXS1047 |

| Seq. ID No. | Expression | Function |
|-------------|---------------------------------------|---|
| 50 | Overexpressed in ovarian tumor tissue | Human homolog to <i>Caenorhabditis elegans</i> cosmid C40H1 |
| 51 | Overexpressed in ovarian tumor tissue | Human homolog to <i>C. elegans</i> cosmid K02D10 |
| 52 | Overexpressed in ovarian tumor tissue | Human homolog to bovine inorganic pyrophosphatase |
| 53 | Overexpressed in ovarian tumor tissue | Human homolog to <i>B. laurus</i> mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex |
| 54 | Overexpressed in ovarian tumor tissue | Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein or others |
| 55 | Overexpressed in ovarian tumor tissue | Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein |
| 56 | Overexpressed in ovarian tumor tissue | Human homolog of <i>R. norvegicus</i> intestinal epithelium proliferating cell-associated mRNA sequence |
| 57 | Overexpressed in ovarian tumor tissue | Homologous to Bruton's tyrosine kinase |
| 58 | Overexpressed in ovarian tumor tissue | dbpB-like protein |
| 59 | Overexpressed in ovarian tumor tissue | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein |
| 63 | Overexpressed in ovarian tumor tissue | Protease, serine, 2 (trypsin 2) |
| 65 | Overexpressed in ovarian tumor tissue | Human annexin IV |
| 67 | Overexpressed in ovarian tumor tissue | Human X2 box repressor |

| Seq ID No. | Expression | Funktion | Module | Cytogenetische Lokalisation | nearest marker |
|------------|---------------------------------|--|----------------------|-----------------------------|--|
| 50 | in Ovariumgewebe überexprimiert | Humanes Homolog zu Caenorhabditis elegans cosmid C40H1 | | 1q22 | WI-7155 |
| 51 | in Ovariumgewebe überexprimiert | Humanes Homolog zu C. elegans cosmid K02D10 | | 7p11.2-p12.3 | Cda1bc08;D7S506-D7S499;; SHGC-17265+11581;D7S499-D7S2429 |
| 52 | in Ovariumgewebe überexprimiert | Humanes Homolog zu Bovine inorganic pyrophosphatase | Pyrophosphatase | 3q26.1 | SHGC-9372 |
| 53 | in Ovariumgewebe überexprimiert | Humanes Homolog zu B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex | | 3q13.12-q13.2 | D3S1310-D3S1575 |
| 54 | in Ovariumgewebe überexprimiert | Humanes Homolog zu Aplysia californica vesicle-associated membrane protein/synaptobrevin binding protein aber anders | | 20q13.33 | SHGC-11512 |
| 55 | in Ovariumgewebe überexprimiert | Humanes Homolog zu Aplysia californica vesicle-associated membrane protein/synaptobrevin binding protein | PRO_RICH; MSP_DOMAIN | 15q25.3-15q26.1 | SHGC-69080 (D15S202/D15S1046, D15S1178) |
| 56 | in Ovariumgewebe überexprimiert | Humanes Homolog des R. norvegicus intestinal epithelium proliferating cell-associated mRNA sequence | PRO_RICH | 1p32.2-p31.2 | SGC34409 |
| 57 | in Ovariumgewebe überexprimiert | Homolog zu Bruton's tyrosine kinase | rrm; PRO_RICH | 10q21.1-q22.1 | WI-11265; D10S581-D10S210 |
| 58 | in Ovariumgewebe überexprimiert | dbpB-like protein | CSD; PRO_RICH | 15q25.3-15q26.1 | AFM282wg5=D15S202 (D15S1046;D15S1187) |
| 59 | in Ovariumgewebe überexprimiert | Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein | PRO_RICH | 2p25.2-p25.1 | |
| 63 | in Ovariumgewebe überexprimiert | Protease, serine, 2 (trypsin 2) | trypsin | 7q35 | SHGC-16894 |
| 65 | in Ovariumgewebe überexprimiert | Humanes Annexin IV | annexin | 2p13.1-p16.1 | SHGC-9858 |
| 67 | in Ovariumgewebe überexprimiert | Human X2 box repressor | | 16q12.1-q22.1 | WI-6174; D16S408-D16S3089;; Cda01g10; D16S419-D16S415 |

| Seq. ID No. | Expression | Function |
|-------------------|---------------------------------------|---|
| 68 | Overexpressed in ovarian tumor tissue | Human transcriptional coactivator PC4 |
| 69 | Overexpressed in ovarian tumor tissue | Human tetratricopeptide repeat protein |
| 70 | Overexpressed in ovarian tumor tissue | Human tax1-binding protein TXBP151 |
| 72 | Overexpressed in ovarian tumor tissue | Human prothymosin alpha |
| 73 | Overexpressed in ovarian tumor tissue | Human profilin |
| 74 | Overexpressed in ovarian tumor tissue | Human pepsinogen C |
| 76 | Overexpressed in ovarian tumor tissue | Human osteopontin |
| 78 | Overexpressed in ovarian tumor tissue | Human non-histone chromosomal protein |
| 79 | Overexpressed in ovarian tumor tissue | Human mRNA for protein disulfide isomerase-related protein P5 |
| 80 | Overexpressed in ovarian tumor tissue | Human mRNA for KIAA0332 |
| 81 | Overexpressed in ovarian tumor tissue | Human mRNA for KIAA0078 |
| 82 | Overexpressed in ovarian tumor tissue | Human mRNA for 90-kDa heat-shock protein |
| 83 | Overexpressed in ovarian tumor tissue | Human major nuclear matrix protein |
| 84 | Overexpressed in ovarian tumor tissue | Human Ku (p70/p80) subunit |
| 85 | Overexpressed in ovarian tumor tissue | Human interferon-induced 17-kDa/15-kDa protein |
| 86 | Overexpressed in ovarian tumor tissue | Human hsc70 gene for 71 kd heat shock cognate protein |
| 88 | Overexpressed in ovarian tumor tissue | Human gamma-interferon-inducible protein (IP-30) |

| Seq ID No. | Expression | Funktion | Module | Cytogenetische Lokalisation | nearest marker |
|------------|-----------------------------------|---|----------------|-----------------------------|---|
| 68 | in Ovariumorgewebe überexprimiert | Human transcriptional coactivator PC4 | | 5p15.1 | SGC32812; D5S477-D5S651 |
| 69 | in Ovariumorgewebe überexprimiert | Human tetralricopeptide repeat protein | | 5q33.2-q33.3 | TIGR-A002Q13; D5S412-D5S422 |
| 70 | in Ovariumorgewebe überexprimiert | Human tax1-binding protein TXBP151 | | 7p14.1-p21.3 | SGC31789; D7S516-D7S632 |
| 72 | in Ovariumorgewebe überexprimiert | Human prolthymosin alpha | | | |
| 73 | in Ovariumorgewebe überexprimiert | Human profilin | profilin | 17p13.3 | |
| 74 | in Ovariumorgewebe überexprimiert | Human pepsinogen C | asp | 6p21.1 | SGC35331; D6S426-D6S271 |
| 76 | in Ovariumorgewebe überexprimiert | Human osteopontin | Osteopontin | 4q13.3-q22.1 | SHGC-9669; D4S1542-D4S1544 |
| 78 | in Ovariumorgewebe überexprimiert | Human non-histone chromosomal protein | HMG14_17 | 21q22.3 | |
| 79 | in Ovariumorgewebe überexprimiert | Human mRNA for protein disulfide isomerase-related protein P5 | thioredo | 2p23.3-p24.1 | SGC31703; D2S287-D2S131; sISG1958; D2S162-D2S287 |
| 80 | in Ovariumorgewebe überexprimiert | Human mRNA for KIAA0332 | | 3p21.1 | SHGC-14798 (D3S4210, SHGC-11985) |
| 81 | in Ovariumorgewebe überexprimiert | Human mRNA for KIAA0078 | PRO_RICH | | SHGC-9647; D7S651-D7S477; WI-14191; D8S269-D8S1799 +2 weitere auf Chr.8 |
| 82 | in Ovariumorgewebe überexprimiert | Human mRNA for 90-kDa heat-shock protein | HSP90 | 4, 11, 1, 6 | SHGC-11305 |
| 83 | in Ovariumorgewebe überexprimiert | Human major nuclear matrix protein | RBD; ZF_MATRIN | 5q31.1 | SHGC-3183 |
| 84 | in Ovariumorgewebe überexprimiert | Human Ku (p70/p80) subunit | | 2q34-q35 | SHGC-11966; D2S2382-D2S164; WI-8140; D2S143-D2S164 |
| 85 | in Ovariumorgewebe überexprimiert | Human interferon-induced 17-kDa/15-kDa protein | ubiquitin | 1p36.31-p36.32 | |
| 86 | in Ovariumorgewebe überexprimiert | Human hsc70 gene for 71 kd heat shock cognate protein | HSP70 | 11q23.3-q25 | D20S113-D20S97 |
| 88 | in Ovariumorgewebe überexprimiert | Human gamma-interferon-inducible protein (IP-30) | | 19p13.13 | SHGC-32638; D19S899-D19S407 |

| Seq. ID No. | Expression | Function |
|-------------|---------------------------------------|---|
| 89 | Overexpressed in ovarian tumor tissue | Human fatty acid binding protein homolog (PA-FABP) |
| 90 | Overexpressed in ovarian tumor tissue | Human enhancer of rudimentary homolog |
| 91 | Overexpressed in ovarian tumor tissue | Human deleted in split hand/split foot 1 (DSS1) |
| 92 | Overexpressed in ovarian tumor tissue | Human decay-accelerating factor mRNA |
| 93 | Overexpressed in ovarian tumor tissue | Human chromosome segregation gene homolog CAS |
| 94 | Overexpressed in ovarian tumor tissue | Human carcinoma-associated antigen GA733-2, human epithelial glycoprotein (EGP) |
| 95 | Overexpressed in ovarian tumor tissue | Human calmodulin |
| 96 | Overexpressed in ovarian tumor tissue | Human Bax alpha |
| 97 | Overexpressed in ovarian tumor tissue | HUMAN antileukoprotease (ALP) |
| 98 | Overexpressed in ovarian tumor tissue | Homo sapiens UDP-galactose-4-epimerase |
| 99 | Overexpressed in ovarian tumor tissue | Homo sapiens mRNA for putative progesterone binding protein |
| 100 | Overexpressed in ovarian tumor tissue | Homo sapiens mRNA for galectin-3 |
| 101 | Overexpressed in ovarian tumor tissue | Homo sapiens monocyte/macrophage 1g-related receptor MIR-7 (MIR cl-7) |
| 102 | Overexpressed in ovarian tumor tissue | Homo sapiens Kunitz-type protease inhibitor |
| 103 | Overexpressed in ovarian tumor tissue | Homo sapiens hCPE-R mRNA for CPE-receptor |
| 105 | Overexpressed in ovarian tumor tissue | Homo sapiens DNA for amyloid precursor protein |
| 106 | Overexpressed in ovarian tumor tissue | Homo sapiens CD24 signal transducer |

| Seq ID No. | Expression | Funktion | Module | Cylogenetische Lokalisation | nearest marker |
|------------|-----------------------------------|---|--|-----------------------------|------------------------------------|
| 89 | in Ovariumorgewebe überexprimiert | Human fatty acid binding protein homologue (PA-FABP) | | 17p11.2 | SHGC-9883 |
| 90 | in Ovariumorgewebe überexprimiert | Human enhancer of rudimentary homolog | ER | 14q22.3-q24.2 | WI-8921; D14S63-D14S251 |
| 91 | in Ovariumorgewebe überexprimiert | Human deleted in split hand/split foot 1 (DSS1) | | 7q21.3-q22.1 | D5S1977-D5S428 (Hs.85215) |
| 92 | in Ovariumorgewebe überexprimiert | Human decay-accelerating factor mRNA | | 1q32.2 | SHGC-11228 |
| 93 | in Ovariumorgewebe überexprimiert | Human chromosome segregation gene homolog CAS | IBN_NT | 20q13 | |
| 94 | in Ovariumorgewebe überexprimiert | Human carcinoma-associated antigen GA733-2, Human epithelial glycoprotein (EGP) | thyroglobulin_1 | 2p15-p21 | AA113218; D2S119-D2S337 |
| 95 | in Ovariumorgewebe überexprimiert | Human calmodulin | EF_HAND_2 | 2p16.3-p21 | WI-9106; D2S391-D2S123 |
| 96 | in Ovariumorgewebe überexprimiert | Human Bax alpha | Bcl-2 | 19q13.3-q13.4 | |
| 97 | in Ovariumorgewebe überexprimiert | Human antileukoprotease (ALP) | wap | 20q13.13-q13.2 | WI-6969 (D20S880, SGC34003) |
| 98 | in Ovariumorgewebe überexprimiert | Homo sapiens UDP-galactose-4-epimerase | 3Beta_HSD | 1p36.11 | SHGC-11459 (RH420-D1S3295) |
| 99 | in Ovariumorgewebe überexprimiert | Homo sapiens mRNA for putative progesterone binding protein | | 4q31.1 | SHGC4-275 |
| 100 | in Ovariumorgewebe überexprimiert | Homo sapiens mRNA for galeclin-3 | Gal-bind_lectin | 14q12-q22.3 | D14S276-D14S66 |
| 101 | in Ovariumorgewebe überexprimiert | Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7) | 7Im_1; G_PROTEIN_RECEPT OR_2; PRO_RICH | 12q14.2-q14.3 | SHGC-33073 |
| 102 | in Ovariumorgewebe überexprimiert | Homo sapiens Kunitz-type protease inhibitor | Kunitz_BPTi; | 19q13.2 | TIGR-A007F08; D19S421-D19S408 |
| 103 | in Ovariumorgewebe überexprimiert | Homo sapiens hCPE-R mRNA for CPE-receptor | PRO_RICH | 7q11.23 | |
| 105 | in Ovariumorgewebe überexprimiert | Homo sapiens DNA for amyloid precursor protein | Kunitz_BPT | 21q21.2-q22.11 | WI-8962; D21S265-D21S260 |
| 106 | in Ovariumorgewebe überexprimiert | Homo sapiens CD24 signal transducer | | 6p21 | AFM115x12; SHGC-13799 - SHGC-32498 |

| Seq. ID No. | Expression | Function |
|-------------|---------------------------------------|--|
| 107 | Overexpressed in ovarian tumor tissue | Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16) |
| 108 | Overexpressed in ovarian tumor tissue | Histone H2B |
| 110 | Overexpressed in ovarian tumor tissue | H. sapiens, gene for membrane cofactor protein |
| 111 | Overexpressed in ovarian tumor tissue | H. sapiens TROP-2 gene |
| 112 | Overexpressed in ovarian tumor tissue | H. sapiens mRNA for Icin protein |
| 113 | Overexpressed in ovarian tumor tissue | H. sapiens mRNA for BiP protein |
| 114 | Overexpressed in ovarian tumor tissue | H. sapiens HE4 mRNA for extracellular proteinase inhibitor homolog |
| 115 | Overexpressed in ovarian tumor tissue | H. sapiens for neutrophil gelatinase associated lipocalin |
| 116 | Overexpressed in ovarian tumor tissue | H. sapiens mRNA for Sm protein G |
| 117 | Overexpressed in ovarian tumor tissue | H. sapiens for glutathione peroxidase-GI |
| 120 | Overexpressed in ovarian tumor tissue | CDC28 protein kinase 2 |
| 121 | Overexpressed in ovarian tumor tissue | B-factor, properdin |
| 122 | Overexpressed in ovarian tumor tissue | Annexin II |
| 123 | Overexpressed in ovarian tumor tissue | ADP-ribosylation factor like 1 |
| 258 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 2 |
| 259 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 3 |

| Seq ID No. | Expression | Funktion | Module | Cytogetische Lokalisation | nearest marker |
|------------|---------------------------------|---|---|---------------------------|---|
| 107 | in Ovariumgewebe überexprimiert | Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16) | | 1q31.1 | SHGC-58249(D1S2602/WI-2775,WI-7265) |
| 108 | in Ovariumgewebe überexprimiert | Histone H2B | histone; Archaeal_histone | 6p21.2-p21.31 | WI-11733; D6S276-D6S439 |
| 110 | in Ovariumgewebe überexprimiert | H.sapiens, gene for Membrane cofactor protein | sushi | 1q32.1-q32.2 | SHGC-12033; D1S456-D1S2891 |
| 111 | in Ovariumgewebe überexprimiert | H.sapiens TROP-2 gene | thyroglobulin_1 | 1p32.2-p32.3 | SHGC-12661; D1S476-D1S220 |
| 112 | in Ovariumgewebe überexprimiert | H.sapiens mRNA for Icdn protein | | 11q14.1 | SHGC-31540; D11S4179-D11S937;; SGC31540; D11D911-D11S1352 |
| 113 | in Ovariumgewebe überexprimiert | H.sapiens mRNA for BiP protein | HSP70; PRO_RICH | 9q33.3-q34.11 | WI-6005; D9S282-D9S260 |
| 114 | in Ovariumgewebe überexprimiert | H.sapiens HE4 mRNA for extracellular proteinase inhibitor homologue | wap | 20q13.2-q13.13 | SGC30446; D20S119-D20S197;; WI-30446 |
| 115 | in Ovariumgewebe überexprimiert | H.sapiens for neutrophil gelatinase associated lipocalin | lipocalin | 9q34 | |
| 116 | in Ovariumgewebe überexprimiert | H. sapiens mRNA for Sm protein G | | 18q21.1 | SHGC-8871 (D18S484;D18S851) |
| 117 | in Ovariumgewebe überexprimiert | H. sapiens for glutathione peroxidase-GI | NLS_BP; GSHPx | 14q24.1 | |
| 120 | in Ovariumgewebe überexprimiert | CDC28 protein kinase 2 | CKS | 9q21.31-q22.1 | SHGC-11955; D9S1812-D9S283;; SGC31294; D9S153-D9S264 |
| 121 | in Ovariumgewebe überexprimiert | B-factor, properdin | VWA DOMAIN; TRYPsin_CATAL; sushi; trypsin | | DXS255-DXS426 |
| 122 | in Ovariumgewebe überexprimiert | Annexin II | annexin | 15q22.1-q22.31 | WI-8600+WI-9161; D15S198-D15S159 |
| 123 | in Ovariumgewebe überexprimiert | ADP-ribosylation factor like 1 | arf | 12q22-q23.1 | SHGC-12629; D12S1727-D12S78;; WI-7420; D12S346-D12S78 |
| 258 | in Ovariumgewebe überexprimiert | Verlängerung zu Seq ID No: 2 | | | |
| 259 | in Ovariumgewebe überexprimiert | Verlängerung zu Seq ID No: 3 | | | |

| Seq. ID No. | Expression | Function |
|-------------|---------------------------------------|-------------------------------|
| 260 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 4 |
| 261 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 10 |
| 262 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 10 |
| 263 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 25 |
| 264 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 26 |
| 265 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 30 |
| 266 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 34 |
| 267 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 42 |
| 268 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 46 |
| 269 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 47 |
| 270 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 48 |
| 271 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 50 |
| 272 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 52 |
| 273 | Overexpressed in ovarian tumor tissue | Lengthening to Seq. ID No. 56 |

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| Seq ID No. | Expression | Funktion | Module | Cylogenetische Lokalisation | nearest marker |
|------------|------------------------------------|-------------------------------|--------|-----------------------------|----------------|
| 260 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 4 | | | |
| 261 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 10 | | | |
| 262 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 18 | | | |
| 263 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 25 | | | |
| 264 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 26 | | | |
| 265 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 30 | | | |
| 266 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 34 | | | |
| 267 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 42 | | | |
| 268 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 46 | | | |
| 269 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 47 | | | |
| 270 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 48 | | | |
| 271 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 50 | | | |
| 272 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 52 | | | |
| 273 | in Ovariummorgewebe überexprimiert | Verlängerung zu Seq ID No: 56 | | | |

TABLE II

Seq. ID. No.

ORF Seq. ID. No.

| Seq. ID. No. | ORF Seq. ID. No. | ORF Seq. ID. No. | ORF Seq. ID. No. | ORF Seq. ID. No. | ORF Seq. ID. No. | ORF Seq. ID. No. |
|--------------|------------------|------------------|------------------|------------------|------------------|------------------|
| 1 | 124 | 125 | 126 | 127 | 128 | 129 |
| 2 | 130 | 131 | | | | |
| 3 | 132 | | | | | |
| 4 | 133 | 134 | | | | |
| 5 | 135 | | | | | |
| 6 | 136 | 137 | | | | |
| 7 | 138 | 139 | | | | |
| 8 | 140 | 141 | | | | |
| 9 | 142 | 143 | | | | |
| 10 | 144 | 145 | | | | |
| 12 | 148 | 149 | | | | |
| 13 | 150 | 151 | 152 | 153 | | |
| 15 | 155 | 156 | 157 | | | |
| 16 | 158 | 159 | 160 | | | |
| 18 | 163 | 164 | | | | |
| 19 | 165 | | | | | |
| 20 | 166 | 167 | | | | |
| 21 | 168 | 169 | | | | |
| 22 | 170 | 171 | 172 | | | |
| 23 | 173 | 174 | | | | |
| 24 | 175 | 176 | | | | |
| 25 | 177 | 178 | | | | |
| 26 | 179 | | | | | |
| 27 | 180 | 181 | | | | |
| 28 | 182 | 183 | 184 | | | |
| 29 | 185 | 186 | | | | |
| 30 | 187 | 188 | | | | |
| 31 | 189 | 190 | 191 | | | |
| 32 | 192 | 193 | 194 | 195 | 196 | |
| 33 | 197 | 198 | 199 | | | |
| 34 | 200 | 201 | | | | |
| 35 | 202 | 203 | 204 | | | |
| 36 | 205 | 206 | 207 | 208 | | |
| 38 | 210 | 211 | | | | |
| 39 | 212 | 213 | 214 | 215 | | |
| 40 | 216 | | | | | |
| 41 | 217 | 218 | | | | |
| 42 | 219 | 220 | 221 | | | |
| 43 | 222 | 223 | 224 | 225 | | |
| 44 | 226 | 227 | | | | |
| 45 | 228 | 229 | 230 | 231 | 232 | |
| 46 | 233 | 234 | 235 | | | |
| 47 | 236 | 237 | 238 | | | |
| 48 | 239 | 240 | | | | |
| 49 | 241 | 242 | | | | |
| 50 | 243 | 244 | 245 | | | |
| 51 | 306 | 307 | | | | |
| 52 | 246 | | | | | |
| 53 | 247 | 248 | 249 | | | |
| 54 | 250 | 251 | | | | |

Seq. ID. No.

ORF Seq. ID. No.

| | | | |
|-----|-----|-----|-----|
| 55 | 252 | 253 | 254 |
| 56 | 255 | 256 | |
| 57 | 257 | | |
| 258 | 274 | 275 | |
| 259 | 276 | 277 | |
| 260 | 278 | 279 | |
| 261 | 280 | 281 | |
| 262 | 282 | 283 | |
| 263 | 284 | 285 | |
| 264 | 286 | 287 | |
| 265 | 288 | 289 | |
| 266 | 290 | 291 | |
| 267 | 292 | 293 | |
| 268 | 294 | 295 | |
| 269 | 296 | 297 | |
| 270 | 298 | 299 | |
| 271 | 300 | 301 | |
| 272 | 302 | 303 | |
| 273 | 304 | 305 | |

The inventive nucleic acid sequences Seq. ID Nos. 1-123 and 258-273 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 124-257 and 274-307 are described in the following sequence protocol.

Sequence Protocol**(1) GENERAL INFORMATION:****(i) APPLICANT**

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Ovarian Tumor Tissue

(iii) Number of sequences: 284

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

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tatgggtagg tccgggttttc caacttgcca aacgtatggg gaagcccggg gatggcttcc 120
ataaattttc cagcggatta tggcattcct tccaggaaat acctcttggt aaaggcctgc 180
ttgcaaatat gcatttccaa acttgaaata taggtgtgaa cagtgtgtac cagtttaaa 240
ctttcacttc atttctgttt ttttaattaag gatttagaag ttcccccaat tacaactgg 300
ttttaaatat tggacatact ggttttaata cctgctttgc atattcacac atggtcaact 360
gggacatgtt aaactttgat ttgtcaaatt ttatgctgtg tggaatacta actatatgta 420
ttttaactta gtttaaatat tttcattttt ggggaaaaat cttttttcac ttctcatgat 480
agctgtttata tatatatgct aaatctttat atacagaaat atcagtactt gaacaaattc 540
aaagcacatt tgggttatta acccttgctc cttgcatggc tcattagggt caaattataa 600
ctgatttaca ttttcagcta tatttacttt ttaaagtgtt gagtttccca ttttaaaatc 660
taaactagac atcttaattg gtgaaagttg tttaaactac ttattgttgg taggcacatc 720
gtgtcaagtg aagtagtttt ataggatagg gttttttctc ccccttcacc aggggtgggtg 780
gaataagttg atttgcccaa tgtgtaatat ttaaactgtt ctgtaaaata agtgtctggc 840
catttgggtat gatttctgtg tgtgaaaggt cccaaaatca aaatggtaca tccataatca 900
gccaccattt aaccttctct tgttctaaaa caaaaaccaa agggcgctgg ttggtagggt 960
gaggtggggg agtattttta tttttggaat ttgggaagca gacagcttta ctttgaagg1020
ttggaacagc agcactatac atgaaatata aacaaaaaac ctttactgtt tctaaatttc1080
ctagattgct attatttggt tgtaaagttga gtattccaca gaaagtggta attatctctt1140
ctctcttctc ccattagaaa attaggtaaa taatggattc ctataatggg agcatcaccal200
cttattaaaa cacacataga atgatgaatt aaaaaagttt tctaggattg tcttttattcl260
tgccacattt attgataaac agtgaaggaa tttttaaaaa atttttaaga attgtttgtcl320
acgtcatctt tagaaatggt ctacctgtat atggtaatgt ccagttttta aaatattgga1380
catcttcaat cttaaacatt tctatttagc tgattggttc tcacatatac ttctaaaaga1440
aacttttatg ttataagagt tactttttgg ataagattta ttaatctcag ttacctacta1500
ttctgacatt tttaggaagg ggtaatgtt tttaatgatg gataaacttg tgcgtggtt1560
ttggatctta tgatgctgag catgttctgc actggtgcta atgtctaata taattttata1620
tttacacaca tacgtgctac ccagagatta atttagtcca tatgaactat tgacccattg1680
ttcattgaga cagcaacata cgcactecta aatcagtgtg tttagacttt tcaagtatct1740
aactcatttc caaacatgta ccattgttta taaacctctt gatttccagc aacatactat1800
agaaaaacacc tgctactcaa aacacaactt ctcagtgtca tccattgctg tctgtagaga1860
caacatagca atatctggta tgttgcaagc tttcaagata gcctgaactt aaaaagttgg1920
tgcattagtt gtatctgatg gatataaatt tgcctcctag ttcactttgt gtcaagagct1980
aaaactgtga acctaaacttt ctcttatttg tgggtaataa ctgaaaataa agattttatt2040
tcatgctcac ttcttaaaaag tcataaaaaac aatcaaatag gatcatgttt attgtcatgt2100
gtttctgtgt ttctgacctg tgtgcacacc cctgtgtgtt tataattttt aaattgaatt2160
ttatatgggg tttttatttg ctaaaaacca ggctgttgaa tcacatttgg gaagggtact2220
tatcttaatg actaatgact taattgggaa agttgaattc ttgtaaaata caaaatccaa2280
ggacttcttg ggatttaatc taattgtcac ttcgttaggc agatgcactt ttttggataa2340
tggaaagtta agcataccga atgctacttt tggttgacaa acgggcctaa tagtccgggg2400

```


(2) INFORMATION ON SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 798 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
gcctatattg gaagcagaca gcgatactga tgacattgac cacagagtta cagaggaaaag 60
ccatgaagag ccagcattcc agaattttat gcaagaatcg atggcacaat actggaagag120
aaacaataaa taggagactt tagcacactt cacttgtttc tagaagtcca gaattttgga180
cctccacgtg aaagaactgt tcttacctct gaactggggg ctcccataag ggataatttt240
cctcagagta gcaaaagtttc tcttattaga gaaatcttgt gactcagatg aagtcaggga300
tagaagaccc ttggacctgg caggttaatg ctgattattc cttggccttt cccttgatt360
tatgcaagga aggatatact gagctgatac tcttccaagc ctacaacttc aagttttatc420
atttgaactc aagtactttt gctgctgagg aatggaatca aaagaacgta gtctcctggt480
gaccacctca gatctctatt attaggctag atgtatagcc tctactcccc cagcttcttg540
ctcttgaccc tgcactgtaa gttgcccttc tattagcagc caaggaaaag ggaaacatga600
gcttatccag aacggtggca gagtctcctt ggcaatcaac caacgttgct atgaaatatg660
cctcacactg tatagctcat tataggacgt cagggtttgtt gaaaaaagtg ggcaagacat720
gattaatgaa tcagaatcct gtttcattgg tgacttggat aaagactttt taattttaaa780
aaaaaaaaa aaaaaaaaaa                                     798
```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 882 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

attccaaaca tggcggctcc actagggggg atgttttctg ggcagccacc cgggtccccct 60
caggccccgc cgggccttcc gggccaagct tcgcttcttc aggcagctcc aggcgctcct120
agaccttcca gcagtacttt ggtggacgag ttggagtcac ctttcgaggc ttgctttgca180
tctctggtga gtcaggacta tgtcaatggc accgatcagg aagaaattcg aaccggtgtt240
gatcagtgtg tccagaagtt tctggatatt gcaagacaga cagaatgttt tttcttacia300
aaaagattgc agttatctgt ccagaaacca gagcaagtta tcaaagagga tgtgtcagaa360
ctaaggaatg aattacagcg gaaagatgca ctagtccaga agcacttgac aaagctgagg420
cattggcagc aggtgctgga ggacatcaac gtgcagcaca aaaagcccg cgcacatccct480

cagggctcct tggcctacct ggagcaggca tctgccaaaca tccctgcacc tctgaagcca540
acgtgagcaa agggcagagg cagttggcct atgagtgggc tgatgcgtga ggttggccac600
acattccttc ctgtggactt gacatttttg aagaactctt tgccagataa tgagttcatt660
ttagttttat gctcccattg aaaaattttc cactattttt ataagctgtt aatttcttga720
gtactttata acatgtctgt agcttggata aaccaagtaa gtattttttt tttgtcttta780
gcaaagttta gactgtgaat atgatgacac agattctttt ttatggtggc tttgtctgtt840
ttaaattttt gcatgacttt taaaaaaaaa aaaaaaaaaa aa
882

```

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2901 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

actgagtga gatgaaatca ggacactgaa acagaaaaaa attgatgaaa cttctgagca 60
 ggaacaaaaa cataaagaaa ccaacaatag caatgctcag aaccccagcg aagaagaggg 120
 tgaaggggcaa gatgaggaca ttttacctct aacccttgaa gagaaggaaa acaaagaata 180
 cctaaaaatct ctatttgaaa tcttgattct gatgggaaag caaaacatac ctctggatgg 240
 acatgaggct gatgaaatcc cagaaggtct ctttactcca gataactttc aggcactgct 300
 ggagtgtcgg ataaattctg gtgaagaggt tctgagaaaag cggtttgaga caacagcagt 360
 taacacgttg tttgttcaa aaacacagca gaggcagatg ctagagatct gtgagagctg 420
 tattcgagaa gaaactctca gggaagtgag agactcacac ttcttttcca ttatcactga 480
 cgatgtagtg gacatagcag gggaagagca cctacctgtg ttggtgaggt ttgttgatga 540
 atctcataac ctaagagagg aatttatagg cttcctgcct tatgaagccg atgcagaaat 600
 tttggctgtg aaatttcaca ctatgataac tgagaagtgg ggattaaata tggagtattg 660
 tcgtggccag gcttacattg tctctagtgg attttcttcc aaaatgaaag ttgttgcttc 720
 tagactttta gagaaatata cccaagctat ctacacactc tgctcttctc gtgccttaaa 780
 tatgtggttg gcaaatcag tactgtttat gggagtatct gttgcattag gaacaattga 840
 ggaagtgtgt tcttttttcc atcgatcacc acaactgctt ttagaacttg acaacgtaat 900
 tgctgttctt ttccagaaca gtaaagaaa gggtaaagaa ctgaaggaaa tctgccattc 960
 tcagtggaca ggcaggcatg atgcttttga aatttttagt gaactcctgc aagcacttgt 1020
 tttatgttta gatggtataa atagtgcac aaatattaga tggataact atatagctgg 1080
 ccgagcattt gtactctgca gtgcagtgtc agattttgat ttcattgtta ctattgtgt 1140
 tcttaaaaat gtcctatctt ttacaagagc ctttgggaaa aacctccagg ggcaaacctc 1200
 tgatgtcttc ttgctggccg gtatcttgac tgcagtactg cattcactca acgaagtga 1260
 tggaaaatat tgaagtatat catgaatttt ggtttgagga agccacaaat ttggcaacca 1320
 aacttgatat tcaaatgaaa ctccctggga aattccgcag agctcaccag ggtaacct 1380
 aatctcagct aacctctgag agttactata aagaaacct aagtgtcca acagtggagc 1440
 acattattca ggaacttaaa gatatatctt cagaacagca cctcaaagct cttaaatgct 1500

 tatctctggt accctcagtc atgggacaac tcaaatcaaa tacgtcggag gaacaccatg 1560
 ctgacatgta tagaagtga ttaccaatc ctgacacgct gtcagctgag cttcattgtt 1620
 ggagaatcaa atggaaacac agggggaaa atatatagct tccgtccacc atctatgaag 1680
 ccctccacct gcctgacatc aagttttttc ctaatgtgta tgcattgctg aagtcctgt 1740
 gtattcttcc tgtgatgaag gttgagaatg agcgggtatga aaatggacga aagcgtctta 1800
 aagcatattt gaggaacact ttgacagacc aaagggtcaag taacttggct ttgcttaaca 1860
 taaaatttga tataaaacac gacctggatt taatgggtgga cacatatatt aaactctata 1920
 caagttaagt agagcttctt acagataatt ccgaaaactgt ggaaaatacc taagagactt 1980
 ttaaaaaatag gctttcttat atttgatatt tggaaagaaa agccgtaagg tgtatgtaga 2040
 ccacttaatc actaaatata tttgcctata ggactccatt gaatacatta gccattgata 2100
 atctacctgt ttaaatggcc cctgtttgaa ctctcaagct ttgaagacct acctgttctt 2160
 ccagaagaga acgttgaaa tgccatgttt ccttttgcgt gatctctgtt gatggcactc 2220
 tggaaattgt tcagtttaagt catttttagac atagcattta ttatcactgt ggatctctac 2280
 ttgttgggtg ttatgaattc tttgaagaaa tatattttga agaggtgtgg gaggaaggaa 2340
 tacattttat aaaatgttgt agtgaagccc acaattgacc tttgactaat aggagttaa 2400
 agtatgttaa aaatctatac tggacagtta caagaaatta ccggagaaaa gcttgtgagc 2460
 tcaccaaaca aggatttcag tgtagatttt gtctttcttg aacttaaaga aacaaatgac 2520
 aaagtttgaa tggaaaagcc tgctgttgtt ccacatctcg ttgctgttta cattcctttg 2580
 tggagcctac atcttcttaa gctttttagc aggtatatgt tgaacacttc tgtttcatgg 2640
 ttgagacaga atcagaggcc atggatactg acaactgatt tgtctgtttt ttttctctgt 2700
 ctttttccat gactcttata tactgctca tcttgattta taagcaaaac ctggaaaacc 2760
 taaaaataaa gtgtgtgtgt ttatctagaa aaatatggaa aatattgctg ttatttttgg 2820
 tgaagaaaaa caattttgta tagtttattt caatctaaat aaaatgtgaa ttttgtttaa 2880
 aaaaaaaaaa aaaaaaaaaa a 2901

(2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 579 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

aaagaaagag aaagaaagaa aagaagattg tagctagggg gagagtaggt gaaaagatga 60
acaacatgac cgggaagatt tcctaattct accacagcct ggctctacct taagtcttta120
ataaaagctt gactgaaggt accaaggtgt gctgaagtgg aagcaaagtt ctccaaagtc180
cagcatggta gacatcagtg gtgtaacca aggacagacc ccaaggcaag gtgaacctca240
aaaatggaac ctcaagtcta tgcagtccag ctgccctccc caccagaaag tccttggtcc300
agcccaacat cagtgcctct gagtttgttt actagaaaca aaggaagaat ttccttgtaa360

aaatatagac agagtagtcc ctggctttct cctcttgtag gaaggatgga ttctccatt420
ccataccatc ttccccccac actggcccca gaaatactta attcaactat gtgaaaataa480
agattgtttt tggtttgagg gcatagggat ccatttatcc ttattcttta tgaggcacta540
aattagcttt gtatgttatt aaatgtgtct cgtcaatgc 579

```

(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2809 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

gcagggcctc gtgccgtttg cataaatagg ttttctcact cttctttttt tccttctttt 60
atccctcact cctccccccta aacctgtgtt cagcacaatg gactaattct agcattctga 120
tcataaggcc ctccattttc ctaatgtgtt tcaaggaatc tttttaggaa aaatatccag 180
attattcatt cacttttttt agtatctact aacaactcct ttttttctct agagagttat 240
gaaggaaacag gttgtccttg tctggagtca agctaaacac atgatttggt ttatcgagcag 300
ctggagcaga agttgaaaat gtctttctgt gagacagtaa tttgctactg aagctttatg 360
gcttgtttgc actgattact ccaggatcca aaaacttggg gaaagtcact gaaacactca 420
aggcaaatata ctttacagcc ctgagtgctt gtcaccatag tttgcataat gaatatgaat 480
cccattgggtg tgtgatgtag gaaatcctgt agttgtattt tcttgaactg aaatatttga 540
ctcaaaataa ttaagactca ttgtcatttt tcatcttggc attatttggtg acaagttgac 600
atattaaatc tctttgtctt ctggtaagct tagcttttaa aatgcatttt ccttgtcct 660
gtctttaact agatatacat gcttatattt atagtgggtt tcacagacta taaaattgaa 720
tgtatgaaat ttttatttat atcagtgctt ttaataatga agatattttt ggagtaatgg 780
tgctgtcttg tagcgagtta ttaatcatag taagattttt ttctcttcat ttgctttttt 840
tgtttcatat taacaatttt ttttttacac ggacacaacc ctctgacagt ctttccaaat 900
attaaaatca tttgaatatg tatgtgtgta tctgaacact gctcaagcca tcaagcagtc 960
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ttttatttcc tgacctagca tcccttggat ttctgagttt cagttcagat ttagatgac1080
aatataagct gccttccgaa attgtcaaca tctgaatgtt aagtcattt tcccatggall140
agaagcccgt agttccatga agtatggatt accatttgta tttttcacta acagtaaatg1200
tatttttctt attaatgtgt tgcttagga atgatgaatt acattttttg ttcttcttal260
ccataaacat ctgcattcct cagctcagcc ttcttgtat gttgtttctt tataaatggt1320
tgagctgctg atgcaggat tgccaagcta acagtacaaa tcatttttaa gaggaagctg1380
gcgcgtatgg cagccgagga gcacactctg caggacactg gacaagacag taaatattcal440
acttttaatg ctgattaaag gagtataagg aaagaatacg taggtatata taattggtgal500
gacaaatatt cactttattt atattttata tattattttt ttaatttggg aaatactatc1560
cagttttgta gttgtccttg ttgatttggt tgatattaaa gtattagtaa taattgccag1620

gaaactatca ttagggaggg tttagtgtgt tgctgtttgg actgggaggg atgattttaa1680
tttagtgcta gaaaccaatt ttagtgactg cacagtatat catttgctag acagaaggta1740
gctataaaag taccctgtaa gtcatatcaa aaaagttcag aggaagatta gtaaatattt1800
atcaataaaa ataaacattt tgtttttcta atatcttaac atatcctccc ctttaggaggg1860
aagaacgtgc aaaacgtgag gagctagagc gaatactgga agagaataac cgaaaaattg1920
cagaagcaca agccaaaactg gccgaagAAC agttgagaat tggtgaagaa caaagaaaal980
ttcatgagga aaggatgaaa ctagaacaag aacgacaacg tcaacaaaaa gaagaacaaa2040
aaattatcct gggcaagggg aagtcaggc caaaactgtc cttctcatta aaaacccagg2100
attaaattgc aaactctgaa ctttttacaa agaaaaatgg aaaaactttg tatggtagct2160
tcattgtgaa gtggtttttt gttttgttt ttgttttttt aatttgtaaa atctggaaag2220
ttagcttggt ctaatagggg ctatgctctg caattccctt tttttttttt ttttttctt2280
ccactaagtc aaatccttat cagatcattg ttgtattcta aggagtgcag tatttttcac2340
ctgtttggat tctatattag tggctcgagg aagagcagat cacattgtaa aactatggat2400
ggctctgataa ggcttttact gaocccactg acttcagagt tatactctgt ttgctacatc2460
ataatgctgg ttttgcgtgac tttttgtttt tttatatatt tataaaaaaa gaaaaagttg2520
gtgattgcat tgggaaattc ccagggtatt actggacctt tgtggtgtat tggttaaacca2580
gtgtccttgt gatactgttg ctcttgatgt tcttgatata ggtaaggaaa cagttggtca2640
actctgatac aaagtatata tacagttcag tattgtctct gttcattttg tttttatttc2700
attgacaaaa tcaaacagc attcccatg gtgtaaataa atgattttgc tgaataaagt2760
aaagtcttaa attcaaaaaa aaaaaaaaaa gaaaaacaaa aaaaaaaa 2809

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(2) INFORMATION ON SEQ ID NO. 7:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 910 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

agttcggcac agagaaagta ttttaaccta cctgtagaga tcctcgatcat ggaaagggtgc 60
caaactgttt tgaatggaag gacaagtaag agtgaggcca cagttcccac cacacgaggg120
cttttgtatt gttctacttt ttcagccctt tactttctgg ctgaagcatc cccttggagt180
gccatgtata agttgggcta ttagagtcca tggaacatag aacaaccatg aatgagtggc240
atgatccgtg cttaatgata aagtgttact tatctaataa tcctctagaa agaaccctgt300
tagatcttgg tttgtgataa aaatataaag acagaagaca tgaggaaaaa caaaagggtt360
gaggaaatca ggcataatgac tttatactta acatcagatc ttttctataa tatcctacta420
ctttgggttt cctagctcca taccacacac ctaaacctgt attatgaatt acatattaca480
aagtcataaa tgtgccatat ggatatacag tacattctag ttggaatcgt ttactctgct540
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aaattgggtt ctttaaaatg ctttgggtggc acttttgtaa acagattgct tctagattgt660
tacaaaccaa gcctaagaca catctgtgaa tacttagatt tgtagcttaa tcacattcta720

gacttctgag ttgaatgaca aagcagttga acaaaaatta tggcatttaa gaatttaaca780
tgtcttagct gtaaaaatga gaaagtgttg gttgggttta aaatctggta actccatgat840
gaaaaaqaat ttattttata cgtgttatgt ctctaataaa gtattcattt gataaaaaaa900
aaaaaaaaaa                                     910

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(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1447 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

gcgacggcgg cttagaaagt gcttctgga gcgcagacga ggcatgaat catgtgacgg 60
tggtctgagg aggaacctgt ctttaaagct gtccctgaag tgacagcggg gagaaccagg 120
cagcccagaa accccaggcg tggagattga tcctgcgaga gaaggggggt catcatggcg 180
gatgacctaa agcgattctt gtataaaaag ttaccaagtg ttgaagggtt ccatgccatt 240
gttggtgcag atagagatgg agtacctgtt attaaagtgg caaatgacaa tgctccagag 300
catgctttgc gacctgggtt cttatccact ttgccccttg caacagacca aggaagcaaa 360
cttgactttt ccaaaaataa aagtatcatc tgttactata acacctacca ggtgggtcaa 420
tttaatcgtt tacctttggt ggtgagtttc atagccagca gcagtgccaa tacaggacta 480
attgtcagcc tagaaaagga acttgctcca ttgtttgaag aactgagaca agttgtggaa 540
gtttcttaat ctgacagtgg ttccagtgtg taccttatct tcattataac aacacaatat 600
caatccagca atcttttagac tacaataata cttttatcca tgtgtcaag aaagggcccc 660
tttttccaac ttatactaaa gagctagcat atagatgtaa tttatagata gatcagttgc 720
tatattttct ggtgtagggt ctttcttatt tagtgagatc tagggatacc acagaaatgg 780
ttcagtcctat cacagctccc atggagttag tctggtcacc agatatggat gagagattct 840
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ttgtacaata tgcccaggct tgcagaataa agccaacttt ttattgtgaa taataataag 960
gacatatatt tcttcagatt atgttttatt tctttgcatt gagtgaggaa cataaaatgg1020
cttggtaaaa gtaataaaat cagtacaatc actaactttc ctttgtacat attattttgc1080
agtatagatg aatattacta atcagtttga ttattctcag aggggtgctgc tctttaatga1140
aaatgaaaat tatagctaat gttttttcct caaactctgc tttctgtaac caatcagtg1200
tttaatgttt gtgtgttctt cataaaattt aaatacaatt cgttattctg tttccaatgt1260
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agtattttta aaaatataaa aaaaaaaaaa aaaaaataat tttttgttc agactttttc1380
caaaaatcta aacataatta atatactctt tcagccacat gaataaataa tgagtgtttc1440
ttgtaaa
1447

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(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 671 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

agcgcggtga agcgggggtg ggatctgaac atggcgggcg tggtagctgc tacggcgctg 60
aagggcgggg gggcgagaaa tgcccgcgtc ctccggggga ttctcgagg agccacagct120
aacaaggctt ctcataacag gaccggggcc ctgcaaagcc acagctcccc agagggcaag180
gaggaacctg aaccctatc ccgggagctg gaatacattc ccagaaagag gggcaagaac240
cccatgaaaag ctgtgggact ggctggggcc atcggcttcc ctgtgggtat cctcctcttc300
atcctcacca agcggaagt ggacaaggac cgtgtgaagc agatgaaggc tcggcagaac360
atgcggttgt ccaacacggg cgagtatgag agccagaggt tcagggcttc ctcccagagt420
gccccgtccc ctgatgttg gtctgggggtg cagacctgag gagcgctgcg accctcctag480
gctattgact gttaagtcc caggtttggc ccagattcca gttcgtgcct ctgaggtcca540
ccagagggcg catgaaagccc aggctgttgc caaacctac cctgccccac accaaggagc600
ccaccaaagg caaataaagt tattgagtgt ttagtagaaa ggaaaaaaaa aaaaaaaaaa660
aaaagtcgac c

```

671

(2) INFORMATION ON SEQ ID NO. 10:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 803 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:


```

gaagatgagg gaaagaaga gtcaacagct ttgcaaaaaa ctgaaaaa ggaaattttg 60
aaaaaatcag agaaagatac aaatttctaaa gtaaaaccca aaggcaaaagt tcgatggact120
ggttctcgga cacgtggcag atggaaatat tccagcaatg atgaaagtga aggggtctggc180
actgaaaaat catctgcagc ttcagaagag gaggaagaaa aggaaagtga agaagccatc240
ctagcagatg atgatgaacc atgcaaaaaa tgtggccttc caaaccatcc tgagctaatt300
cttctgtgtg actcttgcca tagtggatac catactgcct gccttcgccc tctctgatg360
atcatcccag atggagaatg gttctgccc ccttgccaac ataaactgct ctgtgaaaaa420
ttagaggaaac agttgcagga tttggatgtt gccttaaaga agaaagagcg tgccgaacga480
aagaaagaac gcttgggtgt tgttggtatc agtattgaaa acatcattcc tccacaagag540
ccagactttt ctgaagatca agaagaaaag aaaaaagatt caaaaaaatc caaagcaaac600
ttgcttgaaa ggaggtcaac aagaacaagg aaatgtataa gctacagatt tgatgagtt660
gatgaagcaa ttgatgaagc tattgaagat gacatcaaag aagccgatgg aggaggagt720
ggccgaggaa aagatatctc caccatcaca ggcatcgtg ggaaagacat ctctactatt780
ttggatgaaa aaataataac ggc

```

803

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 828 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

agcacttcca ggctggggtg tttgtttgga ctggagaagg gaggcggcgg gcgaaggcac 60
gtcgagcggg ggagcggcgc tgccgtgtga gatccgcgga ggccgacagg attcgttggc120
tgccgtcccc cgtgctgtgc attgggttaa aaacgacaac caacatcagc catgaaagat180
ccaagtgcga gcagtactag cccaagcatc atcaatgaag atgtgattat taacggtcat240
tctcatgaag atgacaatcc atttgacagag tacatgtgga tggaaaatga agaagaattc300
aacagacaaa tagaagagga gttatgggaa gaagaattta ttgaacgctg tttccaagaa360
atgctggaag aggaagaaga gcatgaatgg tttattccag ctcgagatct cccacaaact420
atggacaaaa tccaagacca gtttaatgac cttgttatca gtgatggctc ttctctggaa480
gatcttgtgg tcaagagcaa tctgaatcca aatgcaaaagg agtttgttcc tggggtgaag540

```

```

tacggaaata tttgagtga cggggccctc ttttggtgga tgtagcaca tttccacact600
gtgaaggcag tattagaaga cttaattgta aaagctctct tgtactgtg ttacacttat660
gcattgccaa agtttttgtt agtcttgcac gcttaataaa agtgctgaga cacttgttac720
ctaagtaaaa agcctgttcc aaaccatttt actgggaaaa taggattggg gccccatggc780
cttggtatgg ggaagaccgc caaggggaag gaaccaccag gcccaagt

```

828

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 552 base pairs
- (B) TYPE: Nucleic acid

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

ttggtttccg ggcgcaacca atgtgggagc tgtaatagta agagcttcct aaccaaagct 60
tggtattacc gtgtgggggt tcgttttttt cgtgggtggt tatttgattt tgattttttt120
ttcttttatg tgatcttttg gaaaacacat tcagaattat atctcgtttc tacttaaattg180
tagtgcttag ggtaattttt ttgtactgaa gtctttattg gtgggtgcat gctactggga240
acaagttttt gtacaaaagc ttcaatcaga atcactgtgc attactgaga ctctgtttat300
cactagcctt ctgtccctcc cgcagaagac tgttggttg aacaaaataa tatgtatttt360
gatttactta aagtgcctgt aaatttccta gggacctgcc acttttgact gtggatcagt420
tgatgtacac ttgtattatt aaagcactca ataaatcact gtggctgata actgcaaaaa480
tggaaccccg acatttgctt tgtgtcctgg tgaccgctgt agccctacgt gcagtgaggc540
cttgtctaatt tc                                     552

```

(2) INFORMATION ON SEQ ID NO. 15:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 993 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

gcgggtattaa tatttaattt atttttttta cttataggtc atgttgatgt ctatgataaa 60
cagatgtttt gcctctgaca gcagaacttc ctttcatttt tctcattcgt tttctttggt120
gggttcattt ttttgaatca accacacttc attattttcta ttaagcaatt tgacaggact180
gttgtagcct gcagtgtagt aaaccttctc atcgaaaact ttccatctt cccttaaaat240
gcttgctaatt gtcaaaagt gttcttgatt cttttgggca ctagaaaatc catcgaaaaga300
ccgtacaaac acagtcattt cggctctatc ttcaatgaag acatctgact ctaaaggcct360
gggtggatca aattgctgtt cagagggaat atacaggga atggtaatgg tagactcact420
aaaaggacct gaaccaggct ccacgtagct tgtcactgga gctgtcatct ttattttcat480
ctctttctcg tttttgcctt gaatgtagct gttcagtttc gtaaagcccc tctggatggc540
tgaatcccag tccatagact ccacggacgt gctgacccac ttggctggtc catagtgtcg600
gatctcataa cttccgggct gggggccggc gtcctccggg gccttccagc ccggcgtctc660
cacagcttg ggcgcgcgt cctcgccgc cccggggtct ggctggagcg gctcggccat720
ggggcgcgctg acgctctggg agcctggtca gccgcgcaga ggccccgcac cccgggcccgc780
ccgcctgctg tgtgcgcgcc ccgcgaggc cccgagtcct cctccgcaga cccggtcct840
cctcccggcc gggtggaga cccgagccca cccgatgcgt ctgcctctgg accgcgagg900
ggcgccgcca ccaaggcggg gccggctcac gaccccgac agctccggc ggagttgcgc960
gtcctgcccc cgcccccccg cggcgacagg gag 993

```

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ctgcacctta gaaaaaaaaa gaaaaaatcaa aaaaaacaaaa aaacaaaaaac aaaaaaagaa 60
ggaaaaatctt ggagggtggg cgtgggaact caggacccca gagtggcgag tgggtgggg 120
agggagagcc tctctccccc tttctgtgt gagaggaact cttagtgtct ggtgcagcta 180
ttaaattgtc aatgtgtcaa gtagcttgtt ttacacgcta caacatagct catttgaac 240
ccattgtata agctgtgtat ttacaaatat aacacaacaa ttttaactttt ccttagaata 300
caaaaaagtc tgcattgtct ggggaactat atgcttttcc atttttaagt. caggactgca 360
atactgattc cagttaatga gcagctaaga tccaatctgt ctaatacagt gaccccttag 420
ccatccgggc ctggcaatat acaatttttt tccccctcca agtttgaac actcccttc 480
cagaaaaggc ttgtgcaaca caggattatt tttaaatgat tctgaatttg aattaacttt 540
ttggagaatt ctgtgatgcc cttagaagaa attggacacg tattgagtgt cacaaagctg 600
gggctgggaa ttgtctgtct aatgtttcat tagacttaag aacctaaaat ttttctcagt 660
tgggtggata aaaccactaa cgcttagaaa ctgttttctc atgcagctat gtttctctta 720
tttatgcctt gaggactaat ttctggtttt ctagctgtta atgcactgtt gaccttcata 780
atgggtgcctt acgcaagcga tcccttctgt gggggtctca tacaggggtg tgggcgatgc 840
atgctttatt aaggctcttg tttcacctgg cagtgtactg tatcaacgta taatacagaa 900
aaaaaatctc ttttaaggctc tcttcacaa agacatagag tgaaactccc tttacatgtc 960
agtatttgtt caacacttta ggcaacttga ctgtcagtgt taaaatggaa aacaggaaa1020
tggaaaaatc tgaccaattc tgccaccttg agactttcat atagaccttg cacaacaatt1080
gtatagatca cacaccggct gtatttaata tghtaacattt tcacacatat taaagatacal1140
gaagtattaa aaaaccccca atgttaatgt atttgcttaa aaggcacaag tttcacatat1200
ctgtctagct atctgttggt aatacagaaa gtatactact tttttaaaaa agtgggcagal1260
attcttgtgt atgtatatat gtgtgtacag tatgtgtatg tgtgtatata tatatattat1320
atatatagat aatatataaa tatttttttt aaggagaaac tagaatgttt agctagaaaa1380
ttccacagcc tgtgaagaaa tatttcaaaa tggccataaa ggaggtaaaa atgaaaaccal1440
taacctaaact tttatagagg ctttatcttt aatttaacga tgtgcggagg actttcttgc1500
ttgaatctgt tccgggctgt ctgctctgtc catcaaattg gcaggctctg aatggggcac1560
cttcggccgt tcagaagtgg cctgaacaga atgctggaac ccaggctgga ctcggaacal1620
ctaaggtttt gattttgaat ttcagcctta ttagaagatc taacctaaaga gtaagctaac1680
cacagggtatt cttttgtaga acacttttta tgcagatgaa gctatttttt ccagcaagtal1740
gattcttcca gtttttccaa ggagtaattt ccccgaattg gcataccacg gcgtggacag1800
ctgatatttc acccagctgc tggcttgtgg gtgtggctct ttgctttata tatatatacal1860
cacatgtgag tctggctggg ctggtatttt gtttgatctt cctggaaaatg agcagtgaact1920
aacgctcaca taactgtttt tttttttatc tgggctgatg aatacattta cctaagaaac1980
tcatttcgtt ttacttaaga ggggaagtgc agttttcttt tggcagttca gaatccaagc2040
acttgatttg ctgggttttg aaaactcctt ttttggcctt ctatgtgctt agccataaca2100
attccattaa gcaagaaggt aagcaaaaaga caaaaaaaa aaagggaaaa aaaaaaaact2160
tgcaagggtc tgtctcactt acgaaacatg tggagctgt ttgcctgggt ggggctgggt2220
accgtacctg tcaatgctg ggattttcca taaatttagc acgggacata aag 2273

```

(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 986 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

gcgcgatata aacagttgga agagaaaatg gtacagcagt tacaagagga tgtggacatg 60
gaagatgctc cttaaaaatc tctgtaacca tttcttttat gtacatttga aaatgccctt120
tggatacttg gaactgctaa attattttat tttttacata aggtcactta aatgaaaagc180
gattaaaaga catctttcct gcattgccat ctacataata tcagatatta cggatgttag240
attgcatctc agtgtraaat ctttactgat agatgtactt aagtaaatca tgaaaattct300
acttgtaact atagaagtga attgtggacg taaaatgggt gtgctatttg gataatggca360
ctaggcagca tttgtatagt aactaatggc aaaaattcat ggctagtgat gtataaaaata420
aaatattctt tgcagtaaaa tattcccttt gttaatgtta tagaaggggg gatacaaaaa480
ggaactaaca atttgtatgg cagtgtcaga tatttttatt ttagtatttc ctgttttgg540
ttatttgcat cttagaagag cataatgaca ttgtttgatg aagcctaatt atgctggact600
gttttgacct ggtttaaccc ttctgatagg tagttgtgga tgctggggat gagaactgaa660
taatctttgc ctggagtgac actacactct agaatttcca ctttggagaa tactcagttc720
caacttgatg ttctgatag aacagacttt acttttctag cccagcattg atctagaagc780
agaggaatcc cagcgccttt taaaagtgtg tatgtgggtt tcttttaaaa agctcctgtt840
tttgaaaagt agaatttatg ggtacaacgt atgttcatta ttgtacata aaataaaacc900
atttaaaaag ttaaaaaaga aaaaaaaaag gggggaaaaa aaaagagaaa aaggaaaagg960
aaaaagaaaa aggagggggag aagaga                                     986

```

(2) INFORMATION ON SEQ ID NO. 19:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 526 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| gcgtctatat | tacatttatt | gacactggat | atttattatc | tggtatatac | caggcaaaaat | 60 |
| ggacacacca | tcaggagata | agacctgtat | cttacgtgta | agatgaaact | tatgcaaaaag | 120 |
| gcacagaaca | aattatttgt | tcacagttac | ttttaactct | ttcagcaatg | cctgagtcct | 180 |
| ctttatagaa | acttcatttt | gctaagttag | caaccattca | tttttttggt | tactcttcat | 240 |
| gtatagtgtt | ctcaagtgtc | tcttcaaata | ctgcataatg | gtatagacca | tttaatattc | 300 |
| caaacataat | ctgaagaact | agaggaatcg | ccatttaattt | catttgtgtt | tgacaaagcg | 360 |
| tcattccaatg | gattaaaaacc | cttcctttttg | gtggcagtg | aacggtatga | tacctaaaaa | 420 |
| | | | | | | |
| gaaaaaaagag | ttaatcacct | ctcctggata | tgaatgctat | tagaagtttg | ttgactttct | 480 |
| ctaaattgat | aattgocctt | ctagatctat | aatgtagaga | gcaaaa | | 526 |

(i) SEQUENCE CHARACTERISTIC:

- (vi) ORIGIN:

- (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

tttttttttt tttttttttt gctgtttttt atttattttg gattgttgtc aaataataat 60
ttatttttaa aaaatctcaa aacatgttca aacacattca gtagcaaga tccaccattg 120
gcacacacat taagaaagca cacacactag gcttctagtt gggctaatta aaatctctat 180
ggctggaaag gtggttggtt gtacttaatt aagctttttt gaagtgcata gctatgcata 240
acagatgagc ttgaaagctg cagagttaa gatagactta atttttcatg attttcccaa 300
agccagtcac gatattttatt taatttggtg tcttcagggt gcaccaatcc catgaagctc 360
aattggatac ttccactgct ttgtcaggta ttcatctgag aacttgacaa tgggtttttgc 420
ccgaagatcg tagagaccaa gaggtttaag aagtcttgac acatctctcc agtctgagg 480
tcttgctacc tcagctgaag gatacttctc cagaaacttc caaagcacag gtattgccat 540
tttgctgag gtccgattga gaaatatagt agcgatgaga agcttccatg gatcatgaaa 600
aagtgtttct tgaacgagat taaaagggtga ccgaggaggt gtccatttct taaaggcttt 660
acgtcggtgg gggctaagag cttctttgtt atatttgctg gaaaaatata ggcttggttt 720
ccttctttct atctgtgttc gtgggatggt atcttcagtg aagtctttcc tggttgggtg 780
gcagttgttg tccatttcag agccacgttt taaaatgtca gtatgcaaat gttctttcct 840
ttccacaact tctaactttt ttccgatttc ttcagattct aaaaagggtat cctcatactt 900
ctcgttgtgt tctgagtcct tggctgaaca aaatttggtt atgatgccag aagttttttg 960
ttcagaacaa aaatttgatc ctgaactcaa tgatctttct ttttttttta caaggctgtt1020
ttcttcaactg gtcacactga gggtctcacc acatgctcca gcatcagaaa tgcagacagt1080
tctatcaagc tgactttttt gtgcaacagg ttcactttca gcatctgctt tattacacac1140
agattctctt ttgctatcac ttgaaacaaa acctgaacag ctcttcttac atcctttttt1200
agttttctta attgggattc ctttcaaaat agtcaccttt cctttgggct ttctaacctt1260
tctgaagtta acatcatcaa caccctcatc ttctttcaaa agcaaagtga tggaaagtaa1320
gttagagagt cctctgctct cctgcaactc tgaactacta cttggcgcca taaacacatc1380
ctttttgcac ttgcttcggg tcttgagggt ccagtttgaa ttgttacttt ggttttgtag1440
atgggatgtc agggctgcca tgctgcagtc tttatatctt gacttgatac cctttttaga1500
aagtacagta aaatcaaaat cttctggctt aagagaagtc tctccatttt tgtgaagata1560
attagcaagt gaacttttgg atctgaactt cagtccttgt gggctagaaa atgatatta1620
aggaaactta ctgctagtaa atagaaggga cttttaaaag aactggacca catctcagat1680
ttctaattaa ttccaaaatg ttgccatagg tatctgtcat ttaaaaatga aaaagagtga1740

```

taaatggcac ttttaaatgg tttcc

1765

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 746 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

gtttttttt gttttcttta aatttggatg tctctacacc actcctgatt tgtaggacta 60
aatagatcta tttattccaa tgcaaattgt gtaacattta tttcttccct gatttttaaa120
aatacttttag tattcttaac tatgtatgtg ccttctctta cactgagttc ttttttgctc180
ctttcagctg ctcacacaat cctgtctgtt ggagtcatag ctgctaattc catattattt240
ctctacacac cttgaacatt tagtgtatta ctggtaccct tctgtgttct aggaaacaaa300
tgaattgcaa actggacttg taacaggatc atacatagag caacaaatta gctactggct360
ttgtaagata gtaagttagg aatttcacag tcatgtctcc aaatttcatg gcagagttta420
aaaaacaata taagactgtg gtaaggatca aacgcaaag caatttgctg tgactaattt480
cctaggactt atttcttat gtaaaacccc tgttctttct ttctgcccac aagacagggt540
acaaagcttt ctaaaacatg ctctcaggtg tccacacctg agacattgct ttgtggatac600
tctcaaaggt gtccacaaag caaaaaaatc agaccaaag ctaagagcaa gtaacttata660
cctcaccacc tggacatggc actggcaaaa gtcacttcag cattagaaca gtaatgtttt720
tgctaaatta ctaaaataat agccgc

```

746

(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 659 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

agcagactca caccagaact acattccctg gccccctgcc tgtgtgcttc tggccaggcc 60
ttggttggca agtctgacct gagaaaagga tctgcagaaa atcagactat gggatcactt120
tgtttgtgca ttgggaatga cattctttcc caccocagga aaacctttgg gactttcaga180
gacattgttg ctagccaacc acatggctcag cctcaaagtt gagaggctca gtaacctctc240
tatccctaga gaattccaaa gtgtggatgt aatttaacta gaaagccatt ggtgactatc300
tgtgatccct tggaaagtat ctatgtttgt tatatcttgc atccaaagcc agagggaaacc360
acaatgacta gtaaaacggt ggtctcaatg cccacttagc ctctgcctct gaatttgacc420
atagtggcgt tcagctgata gagcgggaag aagaaatatg cattttttat gaaaaataa480
atatccaaga gaagatgaaa ctaaatggag aaattgaaat acatctactg gaagaaaaga540
tccaattcct gaaaatgaag attgctgaga agcaaagaca aatttgtgtg acccagaaat600
tactgccagc caagagggtc ctggatgccg acctagctgt gctccaaatt cagttttca 659

```

(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 357 base pairs
- (B) TYPE: Nucleic acid

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
cgcagtgcgc agccgtgggg ctctctcctt gtcagtgcgc gccgcgtgcg ggctggtggc 60
tctgtggcag cggcgggcggc aggactccgg cactatgagc ggcttcagca ccgaggagcg120
cgccgcgccc ttctccctgg agtaccgagt ctctctcaaa aatgagaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggta aggcattcctt gtttttggac240
acagtctctt tactcagatc agctagtctt acatatgaat ttctttatat gtctctcaac300
aagtgcctaa aatgcctcgt tgtgctgtga gtaaaggctt gttgattagg ctggggcg 357
```

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 890 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

cggaggcagc ggaagccga gccaggcgc tgccgcctgg gaagagtagg ttcaagatgc 60
attccgggaa ccggggcgcg gcgcactgcg caggcgcccg gactccgctc agtttccgggt120
gcggcggaaca ccaagtcgc ggaacttaag cattttcggg ttctaggggt gttacgaagc180
tgcaggagcg agatggaggt ggacgcaccg ggtgttgatg gtcgagatgg tctccgggag240
cggcgaggct ttagcgaggg agggaggcag aacttcgatg tgaggcccca gtctggggca300
aatgggcttc ccaaacactc ctactggtg gacctctggc tttcatcct tttcgatgtg360
gtgggtgttc tctttgtgta ttttttgcca tgacttggtc gctgatatct aaattaagaa420
gttgggttctt gagtgaattc tgaaaatggc tacaaacttc ttgaataaag aagacaggac480
tctcaataga agaatttcac atctccaagg gaccttctt ttcattttac actttgttac540
taatttcgag aactctatta attgggtagg atttcaccca ttcctagcta agttcttaaa600
attaaaccct ttgggtcgtg tttaaaaact ttcaaacatc tgatggcttt acaggggctg660
aatataaaag catttgtact taaaggctct gtgtattcat taagaaatat agtaattgtct720
tttaaatgtt taagagttga tcagggttta ctatggatgg caagtaatag ggatgattaa780
taagggggaag gtttttatgg aatttcaaaa gtcaatttat ttcaaaagcg ggggaaaggg840
ttttgagagg agggggggccc aagggtgttc tggggtttgc cgaggagggc 890

```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 651 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

gcccgtatatt gcatactaca tcagcaaaaag gtgttgccgc tttataagcg ggcgctacgc 60
caacctcgagt cgtggtgcgt ccagagagac aaataccgat actttgcttg ttgatgaga120
gcccgggtttg aagaacataa gaatgaaaag gatattggcg aggccaccca gctgctgaag180
gagggccgagg aagaattctg gtaccgtcag catccacagc catacatctt cctgactct240
cttggggggca cctcctatga gagatacgat tgctacaagg tcccagaatg gtgcttagat300
gaatggcctc ctctcgagaa ggcaatgtat cctgattact ttgccaagag agaacagtgg360
aagaaaactgc gcagggaaaag ctgggaacga gaggttaagc agctgcagga ggaacgcca420
cctgggtggtc ctttaactga agctttgccc cctgcccga aggaaggtga tttgccccca480
ctgtggtggt atattgtgac cagaccccg ggcggccca tgtagaaaga gagagacctc540
atcttctcatg cttgcaagtg aaatatgtta cagaacatgc acttgcccta ataaaaaatc600
agtgaatgg taaaaaaaaa agtgccattg tagtatgcaa taataagcgg c 651

```

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1256 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

ctcgagccga attcggtctg agctttcctc tgaccatcca tatccaatgt tctcatttaa 60
acattaccca gcatcattgt ttataatcag aaactctggt cttctgtctt ggtggcactt 120
agagtctttt gtgccataat gcagcagtat ggagggagga ttttatggag aaatggggat 180
agtcttcatg accacaaata aataaaggaa aactaagctg cattgtgggt ttgaaaagg 240
ttattatact tcttaacaat tcttttttca gggacttttc tagctgtatg actgttactt 300

aaactatcta aaatagagca ttttgggtat tttcatctga ccatccatat ccaatgttct 360
catttaaaaca ttacccagca tcattgttta taatcagaaa ctctgggtctt tctgtctggt 420
ggcactttaga gtctttttgtg ccataatgca gcagtatgga gggaggattt tatggagaaa 480
tggtgatagt cttcatgacc acaataaatt aaaggaaaaa taagctgcat tgtgggtttt 540
gaaaaaggtta ttatacttct taacaattct ttttttcagg gacttttcta gotgtatgac 600
tgttaactga ccttctttga aaagcattcc caaaatgctc tatttttagat agattaacat 660
taaccacacat aatttttttt agatcgagtc agcataaatt tctaagtcag cctctagtcg 720
tggttcacat ctttcacctg cattttatct ggtgtttgtc tgaagaagg aaagaggaaa 780
gcaaatagca attgtactat ttgtaccaaa ttttgggat tcattggcaa ataatttcag 840
tgtgtgtgat tattaaatag aaaaaaaaaa tttgtttcc taggttgaag gtctaattga 900
tacgtttgac ttatgatgac catttatgca ctttcaaatg aatttgcttt caaaataaat 960
gaagagcagc tgtccttctt tctcttttta agtgttcagc tgtggcatgc tcagaggttc 1020
ctgtctggat ccagctggag cgggtgtgata ccttctttt tcagctgttc gtgccttctt 1080
tttttgatc caccaaagtg gagacaaata catgatctca aagatacaca gtacctactt 1140
aattccagct gatgggagac caaagaattt gcaagtggat ggtttggtat cactgtaaat 1200
aaaaagaggg cctgggaatt cttgcgattc catctctaaa aaaaaaaaaa aaaaaa 1256

```

(2) INFORMATION ON SEQ ID NO. 27:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 694 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

gtttctaaag gatgtgtaag aaaccagagg taaagggtctc gcgatatctt aagacatccg 60
gcgtagtacg cttcagtgag ccacagcgct agagaagtag gagaagctcg cgagatctgt120
gccgttgccg aggagactag gagggggagg agaggggatc tcgcgaaagg aaagaggtcg180
ggagcgctcg cgagatctcg gaccacccaa cctgaaagggt gcttaggaag ttgaaaggcc240
cagaggaggc ctccggggcaa atggccggag ctggaccgac catgctgcta cgagaagaga300
atggctgttg cagtcggcgt cagagcagct ccagtgtctg ggattcggac ggagagcgcg360
aggactcggc ggctgagcgc gcccgcagc agctagaggc gctgctcaac aagactatgc420
gcattcgcgc gacagatgga cggacactgg tcggctgctt cctctgcact gaccgtgact480
gcaatgtcat cctgggctcg gcgcaggagt tcctcaagcc gtcggattcc ttctctgccg540
gggagccccg tgtgtctggc ctggccatgg taccgggaca ccacatcggt tccattgagg600
tgcagaggga gagtctgacc gggcctccgt atctctgacc acgatggcgc ttacctttca660
gacttcatta aacttatgac cgaaaaaaaa aaaa

```

694

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1927 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

gagagatattt atttttttttt tttttttttt acagaaattg acctttattt gttgtactaa 60
agcctgttta actttttgata caaagtaaca ttttagtaca gaaaatccca gtctgtcagc 120
ttagtacctg tctgtgcaca ctgtaccatc tcagtcccac tctgcctgta acttagaaaa 180
cagcccttac ccccagaggg tctgcgagtt aataccttga gaatagtcta cagtttttca 240
tagtttgtct gagctagaaa acttgtacct gtaaaacaaa ggacagcatt gaggactgaa 300
acttgtctct tttttgaaca actgtgcaag aaaatatatc cttttttaaa aaacatcagt 360
tatggctaaa ctacaatcta gtgtctagaa ttacaaagaa taaaatgaaa tcaaagattt 420
ctcgttagta aaatgaaatg ttaggaacag tattaataaata taggtcctac cccaacgaca 480
cttacacaga gcccagtaca gtacctatta ttaacaggac gcatagctta aggaggaacc 540
acatcaaate ttcagccaga catatctagc ctacagaagt caaaaaaaaa aaaagccccc 600
aaacgaagac acccacactg agtaggggtg atgccgtgag tgctgtaate aagattaaaa 660
agacctcagt ttttcttttt agactgttga tagtgacaat aaccattatg cttcccttaa 720
aagctctcaa ttaaatgtct gaaacatgaa tgttttcata tcaaaaagaa ctgatgtacc 780
tgccaccctc taaaaagttt aagaattacc ctgcaaacat tgcaactgat aaggctgtca 840
cgacttacag agcctaagga ggacccaatg gcaggcatca gcacagctga acaccacctg 900
gaccccaactg cagccctgcc cacgcagctc tcacggagca gacacagtcc tcaagtaata 960
agcacagatg gaggagaaac gagaggctgt ggaaggcagg agagaaaggc cgagagacga 1020
gtttgttaaga atgccaagt cacttccccc attgtgggag gaaaatgcca aaggcactgg 1080
ttctgctgcc acaggcagtc tgagcacctg gagttgtgac gtccctccag gagagggtgc 1140
accaaggagc aggaggtttg tcaaaagctt ggtcccacca acaagaacct cccaaagcaa 1200
agcagccccc attgaggttc caaggtcgtt ttgctgaaga cgggaacgaa accaacacca 1260
aagcgacagg ggggtgacag aggggacagg ggctgggcac cggcaacatg gagccgttca 1320
agtaaacata aaccacaaaa tacttagaaa aggcttgtaa acgagtgatc cgaaagggtc 1380
tctttgcagc atctctgate agctggctaa agaaagggtg gtgctgaacc cgtctttagt 1440
gttatctgtt ttgtgttaaa gcacacgtgt gacacgggca gagtgtgtgg gcctgggcct 1500
ggatcgcacg cagccgtggc cctctgtcta caaaggaggt gcttctgggt cctgggtccg 1560
gatccttccc ccgcatgttc atagacggac agacttctac tttcagtcgc tagaaaagag 1620
ctgagctctg tgctccctca ggcggccagc tgcagtcac cacagcacag cattctccta 1680
gagcgggcag gctggaatcc acaggacttt atttgttct tgattgacca ttgccaagat 1740
ctgagtgcaa atgcttgaca gggctcctcc ctggatgacc cctgcaaaaag agccccccag 1800
acacgtcatt cagctcagag taagacccca gggttgaggc aaggcagtag agcttgcaat 1860
ctttctactg tgtggctgtc tgctttgtgc tccttggcac tctgctccat cccacctga 1920
ctctcct

```

(2) INFORMATION ON SEQ ID NO. 29:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 672 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
gcctttttat tttttttttt tggtcgttat gctgcattta ttatgagaat caacagtcaa 60
cagttaatga ttgactaact cttgttggtc actctggaca ttaacgaaaa agactggaat120
agggctacag cgtgtctttt atgctacacg gggtatgctt ggactctgac tcccagcagc180
aggtagattc aggaattcat ggcagtgcac ttcacatca tgggaaacac cttccctttt240
cttcaggatt ctctgtagtg gaagagagca cccagtgttg ggctgaaaac atctgaaagt300
agggagaaga acctaaaata atcagtatct cagaggggtc taaggtgccca agaagtctca360
ctggacattt aagtgccaac aaaggcatac ttctggaatc gccaaagtcaa aactttctaa420
cttctgtctc tctcagagac aagtgcagact caagagtcta ctgctttagt ggcaactaca480
gaaaactggt gttacccaga aaaacaggag caattagaaa tggttccaat atttcaaagc540
tcgcacaaca ggatgtgctt tcctttgccc atttagggtt tcttctcttt cctttctctt600
tgtttagtct tcgttctctt tttcagtttc catcagatct cccctcgtg ccactggaat660
ctcagaggtt gc                                     672
```

(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 269 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

ccgcataccta gccgcgcgact cacacaaggc aggtgggtga ggaaatccag agttgccatg 60
gagaaaaattc cagtgtcagc attcttgccg cttgtggcgc tctctacaa tctggccagg120
gatagcacag tcaaacctgg agccaaaaag gacaggaagg agtctcgagc caaactgcgc180
cagacctctt ccagaagttg gggtgaacaa ctcatctgga ctgagacgta tgaagaagct240
ctatataaat cgagactagc aactaacc 269

```

(2) INFORMATION ON SEQ ID NO. 31:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 604 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

tgcgagggcg ggatagctgt ccaaggtctc cccagcact gaggagctcg cctgctgcc 60
tcttgccgcg ggaagcagc accaagttca cggccaacgc cttggcacta gggccagaa120
tggctacaac agtccctgat ggttgccgca atggcctgaa atccaagtac tacagacttt180
gtgataaggc tgaagcttgg ggcacgtcc tagaaacggt ggccacagcc ggggttgta240
cctcggtggc cttcatgctc actctccgga tctctgctg caaggtgcag gactccaaca300
ggcgaaaaat gctgcctact cagtttctct tctctctgg tgtgttggc atctttggcc360
tcaccttcgc cttcatcctc ggactggacg ggagcacagg gccacacgc ttcttcctct420
ttgggatcct cttttccatc tgcttctcct gcctgctggc tcatgctgtc agtctgacca480
agctcgtccg ggggaggaag cccctttccc ggttggtgat tctgggtctg gccgtgggct540
tcagcctagt ccaggatgtt atcgctattg aatatattgt cctgacgatg aataggacca600
aggt 604

```

(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 781 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

ctttaatgtg cctagagcaa tggaatgggg cactttgggg gcggtggaat tcaagacgct 60
ctggctgaag attcagaagt atctggtaac tctcttttcc ttctgggcat cctctcctct120
gttctaatacc tcccttacac tcattcctgg tccattgcat tctgaccaca tccctaatac180
tggtcaaaaac tattgagtcg tgggcacatt ggatcatgaag gaacaagaag gcaatgagag240
actctcatgc caaccactgc cctgaaagcc ctgctgttca gacagcaaag gggccagcac300
tggccaagct cttatgcttg ctctgaaacc ttcttgggag gactcaatag ggtctccttt360
tgaaagtgtc cctggccttt tgagaaagca gtgtgggtga gggagatggt tctggcaggg420
gocgtgaatg gttgttttct acctgggatt tctttcctgc tttaggagat ctattgggaa480
actgattata accactcggg caccatcgat gcccacgaga tgaggacagc cctcaggaag540
gcaggtttca cctcaacag ccaggtgcag cagaccattg ccctgcggtg tgctgcagc600
aagcttggca tcaactttga cagcttcctg gcttgtatga tccgcctgga gaccctcttc660
aaactattca gccttctgga cgaagacaag gatggcatgg ttcagctctc tctggccgag720
tgctgtgct gcgtgttggt ctgaccgcc aaacttgacc tagaagatgg ggggggcctc780
c

```

781

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 304 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

ggccactgcg ggcagacgcg aggaactgtc gctcgtactc gtgcgcctcg ctttgctttt 60
cctccgcaac catgtctgac aaacccgata tggctgagat cgagaaattc gataagtcgal20
aactgaagaa gacagagacg caagagaaaa atccactgcc ttccaaagaa acgattgaac160
aggagaagca agcaggcgaa tcgtaaggag gcgtgcgcgc ccaagtatgc actgagatgc240
gagaagtgtt gcgtcgaatt tacctgcttg agggggtaaa gttgggaagg tggaaaagg300
gtgg                                     304

```

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1528 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

aattcggatc catgggccac agtggatggc ttgaaatgtg gctgagcgct tcggacactt 60
cggatccatg gtggccaccc caagacgcgc cccagcccgc catggcccgg atcctccggg 120
atcctgcctt ctgtccctgc tcctggccgg gtttgttccg ccgggccggg gacaagagaa 180
gtctaagaca gactgccatg gcggtatgag tggtagcatc tacgagtatg gagccctcac 240
catcgatggg gaggaataca ttcccttttaa gcagtatgca ggcaaatata tcctctttgt 300
caacgtagcc agctactgag gtctgacaga ccaatacctt gaactgaatg cactacaaga 360
agaacttggg ccatttggct tggtcattct gggcttccct tccaaccaat ttggcaaaaca 420
ggagccaggc gagaactcgg agatactccc cagtctcaag tatgttcgac cagggtggggg 480
ctttgtgcct aatttccagc tctttgagaa aggagatgtg aacggggaga aagagcagaa 540
attctacact ttctgaaga actcctgccc tcccactgca gaactcctgg gctcacctgg 600
ccgcctcttt tgggaaccca tgaagatcca tgacatccgc tggaaacttg agaagttcct 660
ggtggggcca gatggcatac cggttatgag ctgggtaccac cggaccacag tcagcaacgt 720
caagatggac atcctgtctt acatgaggcg gcaggcagcc ctgagcgcca gggggagta 780
actgatgccc ccaccctacc cctaccccct gcccatcatg caagggccga ggaggggctc 840
ttcaggaagg aagccacatt cccagtcatt ctacccccac cccagattct ctttcttatt 900
acataaaaga caagcctggc acaactgtgt gtctgaacca ctgtggacac gtgacaattg 960

```

(2) INFORMATION ON SEQ ID NO. 35:

(A) LENGTH: 499 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

| | | | | | | |
|-------------|-------------|------------|------------|-------------|------------|-----|
| ggcagggtctc | agcgctctctc | cccctgctcc | gtctctctgc | agggccagcag | cgcccttggc | 60 |
| cttaggaccc | aacttctctt | accgccatgg | agttcgacct | gggagcagcc | ctggagccca | 120 |
| cttcccagaa | gcccgggtgtg | ggggcgggcc | acgggggaga | tcccaagctc | agtcccacal | 180 |
| aaagttaggg | ccggtcggag | gcaggggcag | gtccgggtcc | aaagcaagga | caccacagct | 240 |
| cttcggactc | cagcagcagc | tccagcgatt | cggacacgga | tgtgaagtcc | cacgctgctg | 300 |
| gttccaagca | gcacgagagc | atcccgggca | aggccaagaa | gccccaagtg | aagaagaagg | 360 |
| agaagggcaa | gaaggagaag | ggcaagaaga | aggaggctcc | ccactgaagg | cgcttgacaa | 420 |
| gggtctatta | aaccttctct | tctgcctacg | agtaccaacc | acctggagct | aagatgctta | 480 |
| ggtggggggg | ggcgcgcga | | | | | 499 |

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gggcacccgt tagttgggaa cagcggaaacg ctggtcccg ggactgagta aggtgtctgg 60
atcggaggga ggttcgggtg ggcacgggc ggctggaaga gctcgactcg tcccgtggg 120
aaagcgcgag tctgagtggg accctggacg acttgacag cggctggcgc agtcattggc 180
gactactgga agtcacagcc aaagaaattc tgtgattact gcaagtgtcg gatagcagac 240
aataggccta gtgttgaatt tcatgaaaga ggaaagaatc ataaggaaaa tgtggcaaaa 300
aggatcagtg agattaaaca gaaaagcctg gataaggcaa aggaagaaga aaaggcatca 360
aaggagtttg ctgcaatgga ggcagctgcc ctgaaagcat accaagagga tttgaaaaga 420
cttggtcttag agtcagaaat tttggagcca agcataacac cagtaaccag cactatccca 480
cctacctcga catcaaatac acagaaagaa aagaaagaga agaagaaaaa aagatccttc 540
aaagggcaga tgggtagaag gcataacctc tgagggttac cattactatt atgatcttat 600
ctcaggagca tctcagtggt agaaacctga aggatttcaa ggagacttaa aaaagacagc 660
agtgaagacc gtttgggtag aagggttaag tgaagatggt tttacctatt actataatac 720
agaaacagga gaatccagat gggagaaacc tgatgatttc attccacaca ctagtgatct 780
gccttctagt aaggtcaatg aaaattcact tggcacccta gatgaatcca aatcatcaga 840
ttcgcatagt gattctgatg gggaacagga agcagaagaa ggaggggtct ctacagagac 900
agaaaagcca aaaataaagt ttaaggaaaa aaataaaaaat agtgatggag gaagtgacct 960
agaaacacag aaagaaaaaa gtattcagaa acagaattca ttaggttcaa atgaagaaaa 1020
atcgaaaact cttaagaaat caaacccata tggagaatgg caagaaatta aacaagaggt 1080
tgagtctcat gaggaggtag atttggaact tccaagcact gaaaatgagt atgtatcaac 1140
ttcagaagct gatggtggcg gagaacccaa agtggtatct aaagaaaaaa cagtcacttc 1200
tcttggagtt atggcagatg gagtggcccc agtcttcaaa aagagaagaa cttgaaaatg 1260
ggaaaatctt aggaaaattt aagggcaacg aggtgatgat ccaatagttt gcagggagag 1320
ctttttgtt acatgctttt tagggaccag aatggggaga ctttttgcca cccccaagt 1380
ttgtcccggt ttttgt

```

1396

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 808 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```
cctctgtcca ctgctttcgt gaagacaaga tgaagttcac aattgtcttt gctggacttc 60
ttggagtcct tctagctcct gccctagcta actataatat caacgtcaat gatgacaaca120
acaatgctgg aagtggggcag cagtcagtga gtgtcaacaa tgaacacaat gtggccaatgi180
ttgacaataa caacgggatgg gactcctgga attccatctg ggattatgga aatggctttg240
ctgcaaccag actcttttcaa aagaagacat gcattgtgca caaaatgaac aaggaagtca300
tgccctccat tcaatccctt gatgcactgg tcaaggaaaa gaagcttcag ggtaagggac360
caggaggacc acctcccaaag ggctgatgt actcagtcaa cccaaacaaa gtcgatgacc420
tgagcaagtt cggaaaaaac attgcaaaaca tgtgtcgtgg gattccaaca tacatggctg480
aggagatgca agaggcaagc ctgttttttt actcaggaac gtgctacacg accagtgtac540
tatggattgt ggacattttc ttctgtggag acacgggtgga gaactaaaca attttttaaa600
gccactatgg atttagtcct ctgaatatgc tgtgcagaaa aaatatgggc tccagtgggt660
tttaccatgt cattctgaaa tttttctcta ctagttatgt ttgatttctt taagtttcaa720
taaaatcatt tagcattgaa acggagaact ctgcgggcta gtaaccacaa ggtacggagc780
aaagatcacc caggtgggaa gaggtgga                               808
```

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1139 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

tttttttttt tttttttttt ttttttgcag caatacctcc tttatttgat ccctgtttat 60
gtccacatat gtactgtatt atcacagatg caactgattt atcatagagc actcagaaaa 120
catggaaaaa tatttttaaa aatcgaataa tcctattcaa gtcaaccagt gttaaccccc 180
gtgtgcttcc tggcagtcctg ttccctcccca tgggagtcac acaaaatgaa aatctcctag 240
aaagagaaat tcctctgtcc tctgacttct tcacttagta cgctgcgacc tccccatgtt 300
gttcaacatc ctcaactcgg agcgtcactg gctggagggtg gtctataaat ggaattggct 360

taactatctc ttcactgaaa ggtggacatt tagggagtggt ccagttttca gctgtcataa 420
acaactgcct tagacggcaa agaattcaca ggtcaatcgt tcccttcgct ttgaacttct 480
tcgcagaccg ttcacttgac cgaagctgga atttgctccc gtaaatgtag gaaataaagc 540
cctcggtttc cacagtgaac acgcagttta gcttggggat aactttcagg cggctcttct 600
tggtgataat tttgaaaatg tgctttgttt cctgtagaag gattcctgta ataccacat 660
aagaggggca tttggatttt gtcactgaaa taatagcccc gtgaagatct gcctttaaga 720
gcttggcctg aatcatctgt ggctgcgtgt ctggcttgag cccactgcac aggtccctga 780
tgtactgttt ccagagttca tggagaggga ggaaaaggct gtatctctgc tgcctctggt 840
taatgtcaaa gagccgcagc tccctccttt gcctggcaga gaagccttg gctttcttct 900
tcttctcctt gcgcttggtg cgggtgaagt actccaggac caccgccttg cgctgcagct 960
ggctcctcgg ggccctgcgg ctcatgcggg gcgtctgcgc ttcaggaagg ccttcacgaal 1020
ggcctcggcc cgctgtgctc ctgaaggctg gacatcggag tcattcgctt cttctgaga 1080
caatgcattg tagatcacac tcttcattct cggaccgctt ccggcgctct ctgatgacg 1139

```

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2177 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

gccccagcgt cccgtcgccg ccggcagcga acagcagcag cagtcagcct tcattcagga 60
aagacagcca gttgctctca tgcgtttatt gtctttcaat gtgcctcata ttaaaaaacag 120
cacaggagaa ccaatatgga aggtactcat ttatgacaga tttggccaag atataatctc 180
tcctctgcta tctgtgaagg agctaagaga catgggaatc actctgcac tcgttttaca 240
ctctgatcga gatcctattc cagatgttcc tgcagtatac tttgtaatgc caactgaaga 300
aaatattgac agaattgtgc aggatcttcg aaatcaacta tatgaatcat attattttaa 360
ttttatttct gctattttcaa gaagtaaaact ggaagatatt gcaaatgcag cgtttagcagc 420
tagtgagta acacaagtag ccaaggtttt tgaccaatat ctcaatttta ttactttgga 480
agatgatatg tttgtattat gtaatcaaaa taaggagctt gtttcataac gtgccattaa 540
caggccagat atcacagaca cggaaatgga aactgttatg gacactatag ttgacagcct 600
cttctgcttt tttgttactc tgggtgctgt tcctataatc agatgttcaa gaggaacagc 660
agcagaaatg gtagcagtga aactagacaa gaaacttcga gaaaatctaa gagatgcaag 720
aaacagtcct tttacagggtg atacacttgg agctggccaa ttcagcttcc agaggccctt 780
attatctcct gttgacagaa acatagattt ggcaactcct ttacatcata cttggacata 840
tcaagcattg gtgcacgatg tactggattt ccattttaa acagggttaatt tggagaagac 900
ttcaggagtg gaaaactctc cagctgggtgc tagaccaaa agaaaaaaca agaagtctta 960
tgatttaact ccggttgata aattttggca aaaacataaa ggaagtccat tcccagaagt 1020
tgcagaatca gttcagcaag aactagaatc ttacagagca caggaagatg aggtcaaacg 1080

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acttaaaagc attatgggac tagaagggga agatgaagga gccataagta tgctttctga 1140
caataccgct aagctaacat cagctgttag ttctttgcca gaactccttg agaaaaaaag 1200
acttattgat ctccatacaa atgttgccac tgctgtttta gaacatataa aggcagaagaal 1260
attggatgta tattttgaat atgaagaaaa aataatgagc aaaactactc tggataaaatc 1320
tcctctagat ataataatcag accctgatgc aggaactcca gaagataaaa tgagggtgtt 1380
tccttatctat tatataagca cacagcaagc accttctgag gctgatttgg agcaatataa 1440
aaaagcttta actgatgcag gatgcaacct taatccttta caatatatca aacagtggaa 1500
ggcttttacc aagatggcct cagctccggc cagctatggc agcactacca ctaaaaccaat 1560
gggtctttta tcacgagtca tgaatacagg atcacagt ttgtatggaag gagtgaagaal 1620
cctgggtttg aaacagcaaaa atctacctgt tactcgtatt ttggacaatc ttatggagat 1680
gaagtcaaac cccgaaaactg atgactatag atattttgat cccaaaatgc tgcggggcaa 1740
tgacagctca gttcccagaa ataaaaatcc attccaagag gccattgttt ttgtgggtgg 1800
aggaggcaac tacattgaat atcagaatct tgttgactac ataaagggga aacaaggcaa 1860
acacatttta tatggctgca gtgagctttt taatgctaca cagttcataa aacagtgtgc 1920
acaacttggg caaaaagtaac acagaagaac cttactatga taatctactt ggaatgtgga 1980
taaatgtaaa aagaagaaaa gttagaagag caatatgttt ccttctctgt aacagtgtcc 2040
taacagtga aatcagagtt atttgttaat ttttaaggaa attatatact taatatgtat 2100
tgatttaaaag aaacatttca gaaataaaat ttcaacattg taaaaaaa gtcggctacc 2160
tacacggata atatcgc
2177

```

(2) INFORMATION ON SEQ ID NO. 41:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 402 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ggcgccaggcc ccagccagct caggctacac tatcccagga tcagcatggc cgtccgccag 60
tgggtaatcg ccctggcctt ggctgccctc cttgttggtg acagggaagt gccagtggca120
gcaggaaaagc tccctttctc aagaatgcc atctgtgaac acatggtaga gtctccaacc180
tgttcccaga tgtccaacct ggtctgcggc actgatgggc tcacatatac gaatgaatgc240
cagctctgct tggcccggat aaaaaccaa caggacatcc agatcatgaa agatggcaaa300
tgctgatccc acaggagcac ctcaagccat gaagtgtcag ctggagaaca gtggtgggca360
tggagaggat atgacatgaa ataaaagatc cagcccaact ga 402

```

(2) INFORMATION ON SEQ ID NO. 42:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

- (vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

cttcttttgc catcccatct ccttggcact gcaccatttc cccaattatt ggccaatccc 60
taggctttct gggttttaca atggttgcga ccacaatcag gctcatagat ggctccaatt 120
taaaaaaaaaa ggtaatggtg atggataaaa taagcagatc aagggaagtg tgctatcata 180
aaataactgt agcttcaaca tcttgagtac cagtttctcg gcagatagta aacatccaat 240
cacaagggat ttttctgaa ggggtgaaag ctggtttgaa aattcttcag tcacagagca 300
gcctacacat gccaaattaga aactgacaga cactagatgt gcttggaaga ttaaacacta 360
cgtacagaaa cagcagttac taagctcctc agtagtttct tgtctttttt aagtttcgct 420
gaatcgacag tttgcacaac gtgctatatt ctgtgggtca aaaccaagta aatactgtgt 480
aaagttggca gattttttcca gctaagatca agaaaaaaca aattttctga taaaacaggt 540
ttagagtcag aaacactctc taaagtgcaa aactgatggc ccacgatctc aaatagctaa 600
aactcctgca gaatggaagg gagagacgtg aaacagggaa ataaattaca gtcagtgtgt 660
gttaatttag gaaaagggaa aaataaacca aactcaagtc ggtaaaagtt atcaaaaat 720
tcaatgatgt agctttcccc actctctgtc acacacgctt gctaacaagt atattaaatt 780
aaggccaaat ttaacctgaa tgcgtttttt tttttctttt tattaagatc tgagatagga 840
acggtcatac ttagtactga aaggcagaca ataaaatggg ccatgaaagg ggggggaaag 900
gtactgtcta ttgttcgagg gattcaacca gagataaaac ctatatacaa gcatgtgtgt 960
agctcgaaat aaaaataaaa ggactatttc atgtcatgac tgcttggttg cttcctcttcl 1020
atatgcattc cctgtgccat tctgtacata ggatgaacca gaaccaaggc catacaaatg 1080
accacaatat ttggcatcat caatatgac ttcaaagaac atttctctca ttttgaaaaa 1140
ggccattcct gtgagcaatg aatcagatcc tgctgatgt tgtgggtccta tccgttccag 1200
ctctaactgt tctgccacct cctgtaatcc acctttgaga tttttctgt catttatgat 1260
gtgaagtacc tcatgaagag ctgcaaaaat ctctaactgt tctgccacct cctgtaattg 1320
cgagtcagtg attgacgaaa taatagtcg 1349

```

(2) INFORMATION ON SEQ ID NO. 43:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 3552 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

atttaattctt cattcttcta ctatccccc aaactaatttc aatatcaaac ctaattaaac 60
acatcaactt cccactgtac accaccacat caatcaaatt ctcccttcatt attagcctct 120
taccocctatt aatatttttt cacaataata tagaatatat aattacaacc tggcactgag 180
tcaccataaa ttcaatagaa cttaaaataa gcttcaaaac tgactttttc tctatcctgt 240
ttacatctgt agcccttttt gtcacatgat caattatata attctcttca tgatatatac 300
actcagaccc aaacatcaat cgattcatta aatatcttac actattcctg attaccatgc 360
ttatccctcac ctccagccaac aacatatttc aacttttcat tggctgagaa ggggtgggaa 420
ttatatcttt cctactaatt ggatgatggg acggacgaac agacgcaaat actgcagccc 480
tacaagcaat cctctataac cgcacgggag acatcggatt cattttagct atagtttgat 540
tttccctaaa cataaactca tgagaacttc aacagattat attctccaac aacaacgaca 600
atctaattcc acttataggc ctattaatcg cagctacagg aaaatcagca caatttggcc 660
tccacccatg actaccatca gcaatagaag gccctacacc agtttcagca ctactacact 720
caagtacaat agtagttgca ggaattttcc tactggctcg attccacccc ctccagacta 780
ataataactt tattttaaca actatacttt gcctcggagc cctaaccaca ttatttacag 840
ctatttgtgc tctaccccaa aacgacatca aaaaaatcat tgccttctct acatcaagcc 900
aactaggcct gataatagtg acgctaggaa taaaccaacc acacctagca ttctacaca 960
tctgtaccca cgcattcttc aaagctatac tctttatatg ctctggctca atcattcata 1020
gcctggcaga cgaacaagac atccgaaaaa taggaaacat cacaaaaatc ataccattca 1080
catcatcatg cctagtaatc ggaagcctcg ccctcacagg aataccattc ctaacagggt 1140
tctactcaaa agacctaatt attgaagcaa ttaatacctg caacaccaac gcctgagccc 1200
tactaattac actaatcgcc acttctataa cagctatgta cagcatacga atcatttact 1260
tcgtaacaat aacaaaaaccg cgttttcccc ccctaatttc cattaacgaa aatgacccag 1320
acctcataaa cccaatcaaa cgcctagcat tcggaagcat ctttgcagga tttgtcatct 1380
catataatat tccaccaacc agcattccag tcttcacaa accatgattt ttaaaaaacc 1440
cagccctaatt tatttcagta ttaggattcc taatcgcaat agaactaaac aacctaacca 1500
taaaactatc aataaataaa gcaaatccat attcatcctt ctcaacttta ctgggggttt 1560
tcccattctat tattcacccg attacaccca taaaatctct caacctaaag ctaaaaaacat 1620
ccctaactct cctagacttg atctggttag aaaaaaccat cccaaaatcc acctcaactc 1680
ttcacacaaa cataaccact ttaacaacca accaaaaagg cttaattaaa ttgtacttta 1740
tatcattcct aattaacatc atcttaatta ttatcttata ctcaattaat ctcgagtaat 1800
ctcgataata ataaaaatac ccgcaaacaa agatcaccca gctactacca tcattcaagt 1860
agcacaacta tatattgccc ctaccccaat ccctccttcc aacataactc caacatcatc 1920
aacctcatac atcaaccaat ctcccaaacc atcaagatta attactcaa cttcatcata 1980
ataattaagc acacaaatta aaaaaacctc tataatcacc cccaatacta aaaaaaccaa 2040
aattaatcag ttagatcccc aagtctctgg atatttctca gtagctatag cagtcgtata 2100
tccaaacaca accaaccatc ccctaaata aattaaaaaa actattaaac ctaaaaacga 2160
tccaccaaac cctaaaacca ttaaacaacc aacaaaccca ctaacaatta aacctaaacc 2220
tccataaata ggtgaaggct ttaatgctaa cccaagacaa ccaacaaaaa ataatgaact 2280
taaaacaaaa atataattat tcattatttc tacacagcat tcaactgcga ccaatgacat 2340
gaaaaatcat cgttgtaatt caactacaga aacaccattc ggatccatga aaaacacacc 2400
cattatttaa aattattaac cactcattca ttgacctacc tgcccatcc aacatttcat 2460
catgatgaaa ctttgggtcc cttctaggag tctgcctaat agtccaaatc attacaggtc 2520
ttttcttagc catacactac acatcagata caataacagc cttttcatca gtaacacaca 2580
tttgtcgaga cgtaaattac gggtgactaa tccgatatat acacgcaaac ggagcctcaa 2640

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tattttttat ttgcttattc cttcatgtcg gacgaggctt atattatgga tcatatacat2700
ttatagaaac ctgaaacatt ggagtaattc tactgttcgc agtcatagcc acagcattta2760
taggctacgt ccttccatga ggacaaatat cattctgagg tgccacagtt attacaaacc2920
tcctatcagc catcccatat attggaacaa ccttagtcga atgaatttga gggggcttct2880
cagtagacaa agccaccttg acccgattct tcgctttcca cttcatctta ccatttatta2940
tcgcgggccct agcaatcgtt cacctcctct tcctccacga aacaggatca aacaacccaa3000
caggattaaa ctcagatgca gataaaattc catttcaccc ctactataca atcaaagata3060
tcctagggtat cctaatacata ttcttaattc tcataaccct agtattatct ttcccagaca3120
tactaggaga cccagacaac tacataccag ctaatccact aaacacccca ccccatatta3180
aaccggaatg atatttccta ttgcatagc ccattctacg ctcaatcccc aataaactag3240
gaggtgtcct agccttaatc ttatctatcc taatttttagc cctaataacct ttcttcata3300
cctcaaagca acgaagccta atattccgcc caatcacaca aattttgtac tgaatcctag3360
tagccaacct acctatctta acctgaattg ggggccaaac agtagaacac ccatttatta3420
tcattggcca actagcctcc atctcatact tctcaatcat ctttaattctt ataccaatct3480
caggaattat cgaagacaaa atactaaaat tatatccata aaaaaaaaaa acgatcgggt3540
gacatatagg gc                                     3552

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(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 601 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

tttttttttt tttttttttt tgcaattcaa atgaacgttt atttctttaa cccacacaga 60
gtaagggcag agcttagaga tgcttgccac agcatttctc atccaggatc acttcctcgt120
tccttcttct ttgctgggag catcttagat ttatatcatt ttctacaaag acaatatcct180
gaatggcagt cgcagggtta tttcaaagtt ggagtcttct caggaagtag gggagactgg240
attcccaagt aatggaattt tcaactgtgat gtctgtgttc tcagtgaatt cttccagaaa300
gccggaggag actgtctcaa catcagtaga gaactcagaa ttctgtttgt ttgcggtcgg360
cgtgaagtcc atgatctgct cagagtcagt gcttaaatca tcatctgtat aatcctctag420
aggagctttt gtccctctgt atgatccag ttggtcaaag actgagttta gtaggtcaat480
gattgaattc tgtagttctt tattgattga aactaattct gacaggggga aagccacagt540
cagaccacag aagacagtga tcaccaggac cttgaaaagc atcatgtctt agtaggggta600
a

```

601

(2) INFORMATION ON SEQ ID NO. 45:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2147 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

agaaggggaa caaaaaaaaa aatatctgaa ttttgaaaaa ccacaaagct acaacactga 60
ccctctcttt tttttgagac ggagttttgc tcttgttacc caggctggag tgcagtggcg 120
tgatcttggc tcaactgcaac ttccgtctcc cgggttcaag tgattctcct gcctcagcct 180
cccaagtagc tgggtttata ggtgcccggc accagaccgc gctaattttt tagttttagt 240
agagacgggg tttcaccacg ttggccaggc tgggtcttaa tgacctctt atttttaact 300
tggtatactg ctattctgcc aaaagacaat ttctagagta gttttgaatg gggtgatttc 360
ccccactccc acaaaactctg aagccagtgt ctagcttact aaaaaaagag ttgtatataa 420
tatttaagat gctgagtatt tcataggaaa gctgaatgct gctgtaaagt gctctttaag 480
tctttttttt ttttaatccc ctcttaatga atgaaactag gggaatttca ggggacagag 540
atgggatttg ttgtatgata aactgtatgt agtttttagt ctttctgttt tgagaagcag 600
tggttggggc atttttaaga tggctggcta ctcttgtttt ccctcatgat aataaatttg 660
tcataactca gtaacatgaa cttgccccta gaggtagtgt ttaataattt tgaaatatta 720
aggtcttgcc aagcttctga tgattcacac ctgtactact gattattaag caggacagac 780
tgagctttct gttgcaataa ccttgaggga gaaagtaatt tctaaatata cagagaggta 840
acttgacctat atatgttgca tctgtgacct cccttcatat taatatttga taaagatttt 900
aatttatgta aaacttctaa agcagaatca aagctcctct tggggaaatg gcaagtcttt 960
aggataggca agaccctgta tgaatagtag caaagcatta ccgcatggtg gagaacacac 1020
tcgattaaaa atgttaagct atctgaaaaa taaaatgtgc aagtcctcag gatggcaca 1080
aacaaggtt aatgcttctt ggggcacatt tcttagaggg ctgtctgagt gtgtaaatat 1140
aatcgacttt tgtttgtgtt acatgacttc tgtgacttca ttgaaaatct gcacaattca 1200
gtttcagctc tggattactt cagttgacct ttgtgaaggt ttttatctgt gtagaatggg 1260
tgtttgactt gttttagcct attaaatttt tattttcttt cactctgtat taaaagtaaa 1320
acttactaaa agaaaagagg tttgtgttca cattaaatgg ttttggtttg gcttctttta 1380
gtcaggcttt ctgaacattg agatatctct aacttagagc tcttcaatcc taagattttc 1440
atgaaaagcc tctcacttga acccaaacca gagtactctt actgcctctt ttctaaatgt 1500
tcaggaaaaa cattgccagt tcagtcctttt caaaatgagg gagaaacatt tgccctgcct 1560
gtaataacaa gactcagtgc ttatttttta aactgcattt taaaaatttg atagtataat 1620
aacaataagg agtaagccac cttttatagg caccctgtag ttttatagtt cttaatctaa 1680
acattttata tttccttctt ttggaaaaaa cctacatgct acaagccacc atatgcacag 1740
actatacagt gagttgagtt ggctctccca cagtctttga ggtgaattac aaaagtcac 1800
ccattatcat cctcctgagt tatttgaaat gatttttttt gtacattttg gctgcagtat 1860
tggttgtaga atatactata atatggatca tctctacttc tgtattttat tattttatt 1920
tagacctcaa ccacagtctt ctttttcccc ttccacctct ctttgccctg aggatgtact 1980
gtatgtagtc atgcactttg tattaatata ttagaaatct acagatctgt tttgtacttt 2040

```

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ttataactgtt ggatacttat aatcaaaact ttactagggt tattgaataa atctagtctt 2100
actagaaaaa aaaaaaaaaa aaaaaaaaaa ctcaagacta gttctctt 2147

```

(2) INFORMATION ON SEQ ID NO. 46:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 623 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

cccacgcgtc cccggaaaacg gcggcgggcg cgacaggacc gaggggcctt agttggtggg 60
caagtcgggg atcccagaaa gagaagcgtg acccggaagc ggaaacgggt gtccgtccca120
gtcccgccct gccagtgagc ttctaccatc atggacctat tggtcgggcg ccggaagacg180
ccagaggagc tactgcggca gaaccagagg gccctgaacc gtgccatgcg ggagctggac240
cgcgagcgac agaaactaga gacccaggag aagaaaatca ttgcagacat taagaagatg300
gccaaagcaag gccagatgga tgctgttcgc atcatggcaa aagacttggt gcgcaccccg360
cgctatgtgc gcaagtttgt attgatgcgg gccaacatcc aggctgtgtc cctcaagatc420
cagacactca agtccaacaa ctgatggca caagccatga aggtgtgcac caaggccatg480
ggcaccatga acagacagct gaagttgcc cagatccaga agatcatgat ggagtttgag540
cggcaggcag agatcatgga tatgaaggag gagaggattg aattgttgca ttgatgatc600
ccgtgggttt tggggaagtt tta

```

623

(2) INFORMATION ON SEQ ID NO. 47:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 781 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

gcgggtatat  tgcaagcttg  aaaaactaaa  agatctgtga  aagatgctgc  caagaagggc  60
cagaaggatg  tctgcatagt  tctggccaag  gagatgatca  ggtcaaggaa  ggctgtgagc  120
aagctgtatg  catccaaagc  acacatgaac  tcagtgtctc  tggggatgaa  gaaccagctc  180
gcggtcttgc  gagtggctgg  ttccctgcag  aagagcacag  aagtgatgaa  ggccatgcaa  240
agtcttctga  agattccaga  gattcaggcc  accatgaggg  agttgtccaa  agaaatgatg  300
aaggctggga  tcatagagga  gatgttagag  gacacttttg  aaagcatgga  cgatcaggaa  360
gaaatggagg  aagaagcaga  aatggaaatt  gacagaattc  tctttgaaat  tacagcaggg  420
gccttgggca  aagcaccag  taaagtgaat  gatgcccttc  cagagccaga  acctccagga  480
gcgatggctg  cctcagagga  tgagggggag  gaggaagagg  ctctggaggc  catgcagtcc  540
cggttggcca  cactccgcag  ctaggggctg  cctacccgc  tgggtgtgca  cacactcttc  600
tcaagagctg  ccattttatg  tgtctcttgc  actacacctc  tgttgtgagg  actaccattt  660
tggagaagg  tctgtttgtc  tcttttcatt  ctctgccag  gttttgggat  cgcaaaggga  720
ttgttcttat  aaaagtggca  taaataaatg  catcattttt  aggaaaaaaa  aaaaaaaaaa  780
a

```

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1714 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

gttgcgacat gcagtgcgcc ggaggaactg tgcctcttga ggccgacgct agggggcccg 60
aagggaact gcgaggcgaa ggtgaccggg gaccgagcat ttcagatctg ctccgtagac 120
ctgggtgcacc accaccatgt tggctgcaag gctgggtgtg ctccggacac taccttctag 180
ggttttccac ccagctttca ccaaggcctc ccctgttgtg aagaattcca tcacgaagaa 240

tcaatggctg ttaacaccta gcaggaata tgccaccaa acaagaattg ggatccggcg 300
tgggagaact ggccaagaac tcaaagaggc agcattggaa ccatcgatgg aaaaaatatt 360
taaaattgat cagatgggaa gatggtttgt tgctggaggg gctgctgttg gtcttgagc 420
attgtgctac tatggcttgg gactgtctaa tgagattgga gctattgaaa aggctgtaat 480
ttggcctcag tatgtcaagg atagaattca ttccacctat atgtacttag cagggaagtat 540
tggtttaaca gcttgtctg ccatagcaat cagcagaacg cctgttctca tgaacttcat 600
gatgagaggc tcttgggtga caattggtgt gacctttgca gccatgggtg gagctggaat 660
gctgggtacga tcaataccat atgaccagag ccaggcccca aagcatcttg cttgggttgt 720
acattctggt gtgatgggtg cagtgggtgc tcctctgaca atattagggg gtccctctct 780
catcagagct gcatggtaca cagctggcat tgtgggaggc ctctccactg tggccatgtg 840
tgcgcccagt gaaaagtttc tgaacatggg tgcacccctg ggagtgggct tgggtctcgt 900
ctttgtgtcc tcattgggat ctatgtttct tccacctacc accgtggctg gtgccactct 960
ttactcagtg gcaatgtacg tgggattagt tcttttcagc atgttccctc tgtatgatac 1020
ccagaaaagta atcaagcgtg cagaagtatc accaatgtat ggagttcaaa aatatgatcc 1080
cattaaactg atgctgagta tctacatgga tacattaaat atatttatgc gagttgcaac 1140
tatgctggca actggaggca acagaaagaa atgaagtgac tcagcttctg gcttctctgc 1200
tacatcaaat atcttgttta atggggcaga tatgcattaa atagtttgta caagcagctt 1260
tcgttgaagt ttagaagata agaaacatgt catcatatct aaatgttccg gtaatgtgat 1320
gcctcaggtc tgcctttttt tctggagaat aaatgcagta atcctctccc aaataagcac 1380
acacattttc aattctcatg tttgagtgat tttaaaatgt tttggtgaat gtgaaaacta 1440
aagtttgtgt catgagaatg taagtctttt ttctacttta aaatttagta ggttcaactg 1500
gtaaactaaaa tttagcaaac ctgtgtttgc atattttttt ggagtgcaga atattgtaac 1560
taatgtcata agtgatttgg agcttttgta aagggaccag agagaaggag tcacctgcag 1620
tcttttgttt ttttaaatc ttaggaactt agcacctggg gttatttgga ttaggtgagg 1680
gagcccggtg ggaacagccg ggtattgggg aaca

```

1714

(2) INFORMATION ON SEQ ID NO. 49:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 831 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

caccgccagc cccctgctctg aggcaccgag aaacgaggag gcccgaggcg agtctccacg 60
tgggtaccgg cgctctcggc gcccgtagcc acccgccccg cggaagccga catctcgagt120
tctggcagaa gcaatttgcg cggcgaggag cggacgggca ggaacccaat aagctgcttc180
gcctcggagc tgaagcccgct actcaagatg gcggctccgg gcgggcgtgg ccagtgacta240
gaaggcgagg cggcgcgga ccatggcggc ggcgggcgac gagcggagtc cagaggacgg300
agaagacgag gaagaggagg agcagttggt tctggtggaa ttatcaggaa ttattgattc360

agacttcctc tcaaaaatgtg aaaataaatg caagggttttg ggcattgaca ctgagaggcc420
catctcgcaa gtggacagct gtgtctttgc tggggagtat gaagacactc tagggacctg480
tgttatattt gaagaaaatg ttgaacatgc tgatacagaa ggcaataata aaacagtgct540
aaaatataaa tgccatacaa tgaagaagct cagcatgaca agaactctcc tgacagagaa600
gaagggaagg gaagaaaaca taggtggggg ggaatggctg caaataaagg ataatgattt660
ctcctatcga cccaacatga tttgtaactt tctacatgaa aatgaagacg aagaagtgg720
agcttcagcc ccagataaat ctttggaatt ggaagaggaa gagattcaaa tgaaccaccg780
gttcaaacgg gggtttggtg aaccggggga acccattgag ccttggggaat t 831

```

(2) INFORMATION ON SEQ ID NO. 50:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 744 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

tgggacccga ggcgcgcgagc aagatggcgg cgcgagtgct gcgcgcccgc ggaggcgctg 60
ggccgggggc ctccctgcagc gggcggcccc ctgcagcctc ctgcccaggc tccggacatg 120
gacatcttcc agcaacagat ctcgagaaga cagctggcta aaatccttat ttgtccggaa 180
agttgatcca agaaaagatg cccactccaa tctcttagcc aaaaaggaaa caagcaatct 240
atacaaatca cagtttcaca atgttaaacc ggaatgccta gaagcataca acaaaatttg 300
tcaagagggtg ttgccc aaaga ttcacgaaga taaacactac ccttgtactt tgggtgggac 360
ttggaacacg tgggtatggc agcaggacca agctgtccac ctctggagggt atgaaggagg 420
ctatccagcc ctcacagaag tcatgaataa actcagagaa aataaggaat ttttggaaat 480
tcgtaaggca agaagtgcac tgcttctctc caggaagaat cagctcctgt tggagtccag 540
tttctggaaat gagcctgtgc caagatccgg acctaatata tatgaactca ggtcttacca 600
actccgacca ggaaccatga ttgaatgggg caattactgg gctcgtgcaa tccgcttcag 660
acaggatgggt aacgaagccg tcggaggatt cttctctcag attgggcagc tgtacatggt 720
gcaccatctt tgggcttaca gggatcttca gaccagggaa gacatacgga atgcagcatg 780
gcacaaacat ggctgggagg aattgggtata ttacacagtt ccacttattc aggaaatgga 840
atccagaatc atgatcccac tgaagacctc gcccctccag taaagctgta ggtttctat 900
gtgcctacat acatttctgt gacaagtatt tgtcgtaaat taattttaat tgtgtatcaa 960
gtgaaaaaga aacactgagg ttttaagctg ctgtatatag cttgtgagaa acctcttttc 1020
tttaaaatct acataatcac aagaaaggaa agaattacag ttggactgat tgtgacagt 1080
ccttgtcgtc ctctttgaaa caccocgtgt tgtccagtat accttataac acttagccac 1140
ttctcccccac cctccagaag ggggtccacgt tgaattctga atcatcttga aaataagatt 1200
ccaaccacaa aaaaaattta gccatttctt tactaaaaaa aacaaaaaaa caaatctgtt 1260
ttataatcac agatttttag acaaatttct tgtatcagga agaaatacaa attttgtcat 1320
gtttctcaag cagtttttct gagtagtttc tgaggaggaa caaattacaa gtgtacccaal 1380
taactgaaaa tgttttaact cactctcatt tgtaagcagt ccacatagta gacaatgggt 1440
tttccaagct ggccaaggta catttaatca gtaaatcagt ttcacatcat gtattgtgat 1500
gtttcaatgt gagacacaaa aacaatggct tgaaacttgt gtatcatatg tgattttgaa 1560
atgaacacct tgaatagcac taatttttat ttgtggtatt tttctataac aaaacaagta 1620
gctctaggaa aagaggtttt attttgtaaa cgatcatttg tgacctcaga cactctctgg 1680
ctaataatctt aataagctca cagcagataa ttctgagatc atgggtgagg ggtgggtgcat 1740
gttgagattt aaattggcat aaagctgcat accttttgct tagctgtttg atttcatttt 1800
ttaatatagt atgccaattt tgtgactgtt accatgtgaa agtctgtttg aaatgaacaa 1860
ttgtctgccc cacaatcaag aatgtatgtg taaagtgtga ataaatctca tatcaaatgt 1920
caaactttta catgtgaatg attttctcaa agaacataga aaagtcaata aaatcctctt 1980
aatttccaca aaaaaaaaaa aaaaaaaaaa aaaaaaa

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2017

(2) INFORMATION ON SEQ ID NO. 52:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 856 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

cgcagtgccg aggcgtgggg ctctctcctt gtcagtcggc gccgcgtgcg ggctgggtggc 60
tctgtggcag cggcgggcggc aggactccgg cactatgagc ggcttcagca ccgaggagcgl20
cgccgcgccc ttctcccttg agtaccgagt ctctctcaaa aatgagaaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggat gtgtttcaca tggtagttga240
agtaccacgc tgggtctaag caaaaatgga gattgctaca aaggaccctt taaaccctat300
taaacaagat gtgaaaaaag gaaaacttcg ctatgttgcg aatttggtcc cgtataaagg360
atatactctg aactatgggtg ccattccctca gacttgggaa gaccacaggc acaatgataa420
acatactggc tgttgtgggtg acaatgaccc aattgatgtg tgtgaaattg gaagcaagg480
atgtgcaaga ggtgaaataa ttggcgtgaa agttctaggc atattggcta tgattgacga540
aggggaaacc gactggaaaag tcattgccat taatgtggat gatcctgatg cagccaatta600
taatgatatc aatgatgtca aacggctgaa acctggctac ttagaagcta ctgtggactg660
gtttagaagg tataagggtc ctgatggaaa accagaaaat gagtttgcgt ttaatgcaga720
atttaaaagt aaggactttg ccattgatat tattaanaagc actcatgacc attggaaaagc780
attagtgact aagaaaaacga atgggaaaag gatcatgttg attgttcaac ttttcggttg840
gccccctcaa gtgtgc                                     856

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(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 540 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```
gcatagacaa agggcctcag aatcgcgag gcgcaattgt gccctgggtc gccaaagatgt 60
cgttcccaaa gtataagccg togagcctgc gcactctgcc tgagaccctc gaccagccg120
aataacaacat atctccggaa acccggcggg cgcaagcgag cggttggtcca taagagcccal180
gctgaaacga gagtacctgc ttcagtacaa cgatcccaac cgccgagggc tcatcgaaaa240
tcctgccttg cttcggttggg cctatgcaag aacaataaat gtctatccta atttcagacc300
cactcctaaa aactcactca tgggagctct gtgtggattt gggccctca tcttcattta360
ttatattatc aaaactgaga gggataggaa agaaaaactt atccaggaag gaaaattgga420
tcgaacattt cacctctcat attaatctg gcaatgatga ctatatgtat tcctgcctaa480
ataaatcatc tattaatcat taataaaaaa aaaaaaaa aaaaaaaa aaaaaagtcg540
```

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1912 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

tgtgtgagggc ccaacagcgg aatcatcgat gcagggggcct gaattaatgt atctgtgatg 60
ttacagcctt tcgattatga tcccaatgag aaaagtaaac acaggttatg gttcagtccta 120
tgtttgctcc aactgacact tcagatatgg aagcagtatg gaaggaggca aaaccggaag 180
accttatgga ttcaaaaactt agatgtgtgt ttgaattgcc agcagagaat gataaaccac 240
atgatgtaga aataaataaaa attatatcca caactgcata aaagacagaa acaccaatag 300
tgtctaagtc tctgagttct tctttggatg acaccgaagt taagaaggtt atggaagaat 360
gtaagaggct gcaagggtgaa gttcagaggc tacgggaggga gaacaagcag ttcaaggaaag 420
aagatggact gcggatgagg aagacagtgc agagcaacag ccccatctca gcattagccc 480
caactgggaa ggaagaaggc cttagcaccg ggctcttggc tctggtggtt ttgttcttta 540
tcgttggtgt aattattggg aagattgcct tgtagaggta gcatgcacag gatggtaaat 600
tggattggtg gatccaccat atcatgggat ttaattttat cataaccatg tgtaaaaaaga 660
aattaatgta tgatgacatc tcacagggtc tgcctttaa ttacccctcc ctgcacacac 720
atacacagat acacacacac aaatataatg taacgatctt ttagaaggtt aaaaatgtat 780

agtaactgat tgagggggaa aagaatgata tttattaatg acaagggaaa ccatgagtaa 840
tgccacaatg gcataattga aatgtcattt taaacattgg taggccttgg tacatgatgc 900
tgattacct ctcttaaaat gacacccttc ctgcctgtgt ggtgctggcc cttggggagc 960
tgagccccag catgctgggg agtgcggtca gctccacaca gtagtcccca cgtggccccc 1020
tcccgcccca ggtgtcttcc cgtgtcttca gttctgtcca agccatcagc tcttgggacl 1080
tgatgaacag agtcagaagc ccaaaggaat tgcactgtgg cagcatcaga cgtactcgtc 1140
ataagtgaag ggcgtgtgtt gactgattga cccagcgctt tggaaataaa tggcagtgtc 1200
ttgttcactt aaagggacca agctaaattt gtattggttc atgtagtgaa gtcaaaactgt 1260
tattcagaga tgtttaatgc atatttaact tatttaatgt atttcatctc atgttttctt 1320
attgtcacaa gagtacagtt aatgctgcgt gctgctgaac tctgttgggt gaactgggtat 1380
tgctgctgga gggctgtggg ctctctgttc tctggagagt ctgggtcatgt ggaggtgggg 1440
tttattggga tgctggagaa gagctgccag gaagtgtttt ttctgggtca gtaataaaca 1500
actgtcatag ggagggaaat tctcagtagt gacagtcaac tctaggttac ctttttaaat 1560
gaagagtatg cagtcttcta gattgttctt ataccacctc tcaaccatta ctcacacttc 1620
cagcgcaccg gtccaaagtc gagcctgacc tccccttggg gacctagcct ggagtcaggal 1680
caaatggatc gggctgcaga ggggttagaag cgagggcacc agcagttgtg ggtggggagc 1740
aagggaaagag agaaactctt cagcgaatcc ttctagtact agttgagagt ttgactgtga 1800
attaatttta tgccataaaa gaccaaccca gttctgtttg actatgtagc atcttgaaaa 1860
gaaaaattat aataaagccc caaaattaaag aaaaaaaaaa aaaaaatact gc 1912

```

(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

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tttttttttt ttttatcgag caagaatctg ttaacagttt tttttttttt tatgttaaat 60
accatgggac aggattgtaa ggatgaaaaa ctcagtcaac aactgcctca caagggataa 120
gaaaaattct gccatgatat tagcaaaggt aaaggaggaa aaatttacac tgtaagaggc 180
accattttcc caaggaatac ctcttgcat ttcctgaatg agtgggatta gcaatctaaa 240
taaatcatat ttcaagaggt aacagcaaca gataaaattt aaagggatta ttaaaataac 300
atttacaaga ctctgaacaa ttcttgaact cttattaaaa ccacaaagaa agaacaattc 360
tttattttatg aatttcataa aggactcaat gtgcaactga catctgctag tgatgatctg 420
gtaatatata acctgtccag tagccgaaca gtttgttttt attgtgtttt ctaaccgtaa 480
gagatcatta aaggcaaagc ctatatgacg ctgtacacac aaaaaaatgg tcaccgtggg 540
ccatactacc aatgaaatgg taggtaaaca aatctttttc tggtaagag aaaaaaaaaa 600
aaaagaaaca gcactctgca tgcttcactc tacaagatga atttccctag aaagaatcca 660

atgaaaaatgg ctgcaattac aacaagaagt gaaggaaagag gactgggtgac attatctctg 720
aaggatgcag ttgaggttga tccaggttta tccgaatgtg ctacctttct gagccttaaa 780
ccttcattct tcaggtgcag attttcttct gatagcttca tcatttctcc ctgaagtcct 840
ttacactctt ccattagttt ccttgtttcg gtatcattaa gtgaaacact gtgtgggttt 900
ggcataggto catcttgctt agatgcattc agtggaaacag ctttgctagg ttccatatca 960
ttcaatttat catcttcatt gggcatttca aatacgcac tcattttgga atccattaat 1020
tcatacaggt ttgctctctt ccacacagct tccatatctg aagtgtttgg tggagcaaaa 1080
attgtctgta ccataaactt gtgtttactc ttttcattcg gatcatagtc aaagggtctg 1140
agcattactg aaacagtcac agttgacctt gggtaataa ttccactgtt gggcctcacal 1200
cagtaccggc gaggtgctgt agtcttcaat ttgaaacaca ctttctatc cgtatggatt 1260
cgcaatttca gatttgtagt gactacatct gtgaaggggc ctttgaattt gaggtctgtg 1320
ggcggatcga ggaccaggat ctgctcgtct tccgcatggc cctgaggcg gagccatcg 1380
gagagacagc gcagagcagg gggcggttg ctgctgggg gcgggggacg atggcgagag 1440
gggaggggga gcgagttcgc atctctctct ttcctgggta gactctgttc aaccacattc 1500
ttatgttggc agatctgctt ccagattgat ttttagagca ccatacctt cacttctctg 1560
attctgattt tgttttgtt tgtttgggtt ttctgaaact taaaatgctg ccccgaaaaa 1620
actatatttt tgagtttgtg ttctgaaagc ctccgtgctg ctggatcttt ggggggaaat 1680
acaggatcct tcagcactga ggtgtttaag atttgcaact agcaatgcaa ttttttctaa 1740
atatggggat atttaccttt attaagaaat tatactaaac attgatgtcc ttgatcattt 1800
tatgttctca tattactttt gattctacta tgattgtgtg gtggtgaaca aagatcattt 1860
caaacaaaaa ctgtaatttt gttatatttg attcaatgga atttacctaa aaaataaaga 1920
ctaaaaatgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
1962

```

(2) INFORMATION ON SEQ ID NO. 56:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

cggetcgagc ggctcgagat tcgaggctcgt ggtgggtcttg gaagagcgtc gaggggggccg 60
tggacgtgga atggggccgag gagatggatt tgattctcgt ggcaaactg aatttgatag 120
gcatagtgga agtgatagat ctggcctgaa gcacgaggac aaactgtgag gtagcggatc 180
tcacaactgg ggaactgtca aagacgaatt aacagagtcc cccaaatata ttcagaaaca 240
aatatcttat aattacagtg acttgatca atcaaagtgt actgaggaaa cacctgaagg 300
tgaagaacat catccagtgg cagacactga aaataaggag aatgaagttg aagaggtaaa 360
agaggagggt ccaaaagaga tgactttgga tgagtgggaag gctattcaaa ataaggaccg 420
ggcaaaagta gaatttaata tccgaaaacc aaatgaaggt gctgatgggc agtggaaaga 480

gggatttgtt cttcataaat caaagagtga agaggctcat gctgaagatt cgggttatgga 540
ccatcatttc cggaagccag caaatgatat aacgtctcag ctggagatca attttgaga 600
ccttggccgc ccaggacgtg ggggcagggg aggacgaggt ggacgtgggc gtggtgggcg 660
cccaaacctt ggcagcagga ccgacaagtc aagtgtctct gctcctgatg tggatgacct 720
agaggcattc ccagctctgg cttaactgga tgccataaga caaccctggt tcccttgtga 780
accctctctg tcaaaagctt tgcatgctta aggattccaa acgactaaga aattaaaaaa 840
aaaaagactg tcattcacac cattcacacc taaagactga attttatctg ttttaaaaat 900
gaacttctcc cgctacacag aagtaacaaa tatggtagtc agttttgtat ttagaaatgt 960
attggtagca gggatgtttt cataattttc agagattatg cattcttcat gaatactttt 1020
gtattgctgc ttgcaaatat gcatttccaa acttgaaata taggtgtgaa cagtgtgtac 1080
cagtttaaaag ctttcacttc atttgtgttt ttaattaag gatttagaag tcccccaat 1140
tacaaactgg ttttaaatat tggacatact ggttttaata cctgctttgc atattcacac 1200
atggtcaact gggacatggt aaactttgat ttgtcaaatt ttatgctgtg tggaaatact 1260
actatatgta ttttaactta gttttaatat ttccattttt ggggaaaaat cttttttcac 1320
ttctcatgat agctgttata tatatatgct aaatctttat atacagaaat atcagtactt 1380
gaacaaattc aaaagcacat ttggtttatt aaccctgtgc tgccctggca tggggcccat 1440
ttgggggtcca aattataa
1458

```

(2) INFORMATION ON SEQ ID NO. 57:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2188 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

gggccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 60
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 120
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 180
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 240
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 300
ccaaacctcc cccacccccc cccctacaag tcacctgggt aagccaacct gaattctact 360
cacctgggag tggaggtatg tatgacagaa tgcgacgagg aggtgatgga tatgatgggt 420
gttatggagg ttttgatgac tatggtggct ataataatta cggctatggg aatgatggct 480
ttgatgacag aatgagagat ggaagaggta tgggaggaca tggctatggg ggagctgggt 540
atgcaagttc aggttttcat ggtggtcatt tgcacatat gagagggttg cttttcgtg 600
caactgaaaa tgacattgct aatttcttct caccactaaa tccaatacga gttcatattg 660
atattggagc tgatggcaga gccacaggag aagcagatgt agagtttgtg acacatgaag 720
atgcagtagc tgccatgtct aaagataaaa ataacatgca acatcgatat attgaactct 780
tcttgaattc tactcctgga ggcggtctct gcatgggagg ttctggaatg ggaggctacg 840

gaagagatgg aatggataat cagggaggct atggatcagt tggagaatg ggaatgggga 900
acaattacag tggaggatat ggtactcctg atggtttggg tggttatggc cgtgggtggg 960
gaggcagttg aggttactat gggcaaggcg gcatgagtg aggtggatgg cgtgggatgt 1020
actgaaagca aaaaacacca catacaagtc ttgacaacag catctggtct actagacttt 1080
cttacagatt taatttcttt tgtattttta gaactttata atgactgaag gaatgtgttt 1140
tcaaaatatt atttggtaaa gcaacagatt gtgatgggaa aatgttttct gtaggtttat 1200
ttgttgcata ctttgactta aaaataaatt tttatattca aacctgatgt gttgatactt 1260
tttatatact agttactcct aaagatgtgc tgccttcata agatttgggt tgatgtattt 1320
tactattagt tctacaagaa gtatgtgtgt gtaattttag aggataatgg ttcacctctg 1380
cgtaaaactgc aagtcttaag cagacatctg gaatagagct tgacaaaata ttagtgtaac 1440
ttttttcttt agttcctcct ggacaacact gtaaatataa agcctaaaga tgaagtggct 1500
tcaggagtat aaattcagct aattatttct atattattat ttttcaaagt tcatttatca 1560
ggcatagctc tgaaacattg atgatctaag aggtattgat ttctgaatat tcataattgt 1620
gttacctggg tatgagagtg ttggaagctg aattctagcc ctgatttttg gagtataaac 1680
ccttcagcac ttgaccgaaa taccataaat gtctccaaaa aattgatagt tgcaggttat 1740
cgcaagatgt cttagagtag ggttaagggt ctgagtgaac caagaattca gtattaatga 1800
cataggtatt tactatggag tataattctc acaattgtat tttcagtttt ctgccaataa 1860
gagtttaaat aactgtataa atgatgactt taataaaatg taagcaacaa gtccatgtca 1920
tagtcaataa aaacaatcct gcagttgggt tttgtatctg atccctgctt ggagttttag 1980
tttaaaagaa ctatatgtag caaggaaaag gtgcttttta attttaatcc ctttgatcaa 2040
tatggctttt ttccaaattg gctaattgat caaaatgaaa cctgttgatg tgaattcagt 2100
tattgaactt gttacttgtt tttgccagaa atgttattaa taaatgtcaa tgtgggagat 2160
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

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2183

(2) INFORMATION ON SEQ ID NO. 58:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ctcgctagtt cgatcggtag cgggagcgga gagcggaccc cagagagccc tgagcagccc 60
caccgccgcc gccggcctag ttaccatcac accccgggag gggccgcagc tgccgcagcc 120
ggccccagtc accatcacccg caaccatgag cagcgaggcc gagaccagc agccgcccgc 180
ggcccccccc ggggcccccg cctcagcgc cgccgacacc aagcccgga ctacgggcag 240
cggcgcaagg agcgggtggc cggcggcct cacatcggcg gcgcctgccg gcggggacaa 300
gaaggtcatc gcaacgaagg ttttggaac agtaaaatgg ttcaatgtaa ggaacggata 360
tggtttcatc aacaggaatg acaccaagga agatgtatgt gtacaccaga ctgccataaa 420

gaagaataac cccaggaagt accttcgcag tgtaggagat ggagagactg tggagtttga 480
tgttgttgaa ggagaaaagg gtgcggaggc agcaaatggt acaggtcctg gtggtgttcc 540
agtccaaggc agtaaatatg cagcagaccc taaccattat agacgctatc cacgtcgtag 600
gggtcctcca cgcaattacc agcaaaatta ccagaatagt gagagtgggg aaaagaacga 660
gggatcggag agtgctcccg aaggccaggc ccaacaacgc cggccctacc gcaggcgaag 720
gttcccacct tactacatgc ggagacccta tgggcgtcga ccacagtatt ccaaccctcc 780
tgtgcaggga gaagtgatgg aggggtgctg caaccagggt gcaggagaac aaggttagacc 840
agtgaggcag aatatgtatc ggggatatag accacgattc cgcagggggc ctccctcgcca 900
aagacagcct agagaggacg gcaatgaaga agataaagaa aatcaaggag atgagaccca 960
aggtcagcag ccacctcaac gtcggtaccg ccgcaacttc aattaccgac gcagacgccc1020
agaaaaacct aaaccacaag atggcaaaga gacaaaagca gccgatccac cagctgagaal080
ttcgtccgct ccgaggctg agcagggcgg ggctgagtaa atgccggctt accatctctal140
ccatcatccg gtttagtcat ccaacaagaa gaaatatgaa attccagcaa taagaaatgal200
acaaaagatt ggagctgaag acctaaagtg cttgcttttt gcccgttgac cagataaatal260
gaactatctg cattatctat gcagcatggg gtttttatta tttttaccta aagacgtctcl320
tttttggtaa taacaaacgt gttttttaa aaagcctggg ttttctcaat acgcttttaal380
aggtttttaa attgtttcat atctgggtcaa gttgagatgt ttaagaactt catttttaat1440
ttgtaataaa agtttacaac ttgatttttt caaaaaagtc aacaaactgc aagcacctgt1500
taataaaggc cttaataaat tgtctttgtg taaaaaaaaaa gggaatat 1548

```


(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1254 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ggaccgcttc ccccgagcca gcagcagcgt ttgacgtcat cgtgcgtgtg gtgcccctgc 60
tgccgggggt ggtgattgga ggaaaccccg tgtctgacgg agggctgtag cctgtgagca 120
gcgagatcca gggacagagt ctcagcctcg ccgctgctgc cgccgccgcc gccagagac 180
tgctgagccc gtccgtccgc cgccaccacc cactccggac acagaacatc cagtcattga 240
taaaaatgag ctggttcaga aggccaaaact ggccgagcag gctgagcgat atgatgacat 300
ggcagcctgc atgaagtctg taactgagca aggagctgaa ttatccaatg aggagaggaa 360
tcttctctca gttgcttata aaaatgttgt aggagcccgt aggtcatctt ggagggtcgt 420
ctcaagtatt gaacaaaaga cggaagggtgc tgagaaaaaa cagcagatgg ctcgagaata 480
cagagagaaa attgagacgg agctaagaga tatctgcaat gatgtactgt ctcttttgga 540
aaagtctctg atccccaatg cttcacaagc agagagccaa agtcttctat ttgaaaatga 600
aaggagatta ctaccgttac ttggctgagg ttgccgtgg tgatgacaag aaagggttg 660
tcgatcagtc acaacaagca taccaagaag cttttgaaat cagcaaaaaa gaaatgcaac 720

caacacatcc tatcagactg gggtggccc ttaacttctc tgggttctat tatgagattc 780
tgaaactccc cagagaaaagc ctgctctctt gcaaagacag cttttgatga agccattgct 840
gaacttgata cattaagtga agagtcatac aaagacagca cgctaataat gcaattactg 900
agagacaaact tgacattgtg gacatcggat acccaaggag acgaagctga agcaggagaa 960
ggaggggaaa attaaccggc cttccaactt ttgtctgcct cattctaaaa ttacacagtl 1020
agaccatttg tcatccatgc tgtcccacaa atagtttttt gtttacgatt tatgacaggtl 1080
tcattgttact tctatttgaa tttctatatt ttccctgtgg gttttatggt tagttttggg 1140
ggagtaggag ccagtttaac gtttggggag tttgtctgtt ttctgtcttt gaggggtgggcl 1200
ccagtatggg gggtgttggt gattttttgt taccagtttt tgagggtgttt ttgg 1254

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(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 954 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

cctcttcttt ttctttttct tctttttttt ttcctttttt ttttttgtga gagcagggtc 60
actttattgg tatagagact gcagagggac caggggcttt agctgttggc agctatgggtg120
tccttaatcc agtcacata gttgtagacc ttgggtgtaga ctccaggcct gttcttctgg180
gcacagccat agccccagga gacaattcct tggagctctc cattggagac cacagggcca240
ccagaatcac cctggcagga atccttgccct ccctcgagga agcccacaca gaacatgttg300
ttggtaatct ttccagggtg ggaggcttca cactcagcct ggctcagcac aggagcatcc360
aggcactgca gctcgtctgg gtagtcggca ccagaactca gagtgttgcc ccagccggag420
atgagggact cgggtgccagc agctggaggg gcagtgaggc gagagatggc ggacacgcgg480
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ctgttgattt tgggggtggcg gatgatcttg gccgcattga tgaactgttc attcccctcc600
aggacttcga tgttggtgctc tcccagcttc acctggatgc gggacttgta gcagtgcct660
gctgacacca cccactgttc gctgatgagg gagccaccgc agaagtggta gccagaattc720
aaggcacact ggtagggggac agaattctcc tcacagatgt agcccccaac gatcttgta780
tcatcatcaa aggggggcagc aacagcagct gcaacaaagg taaggatcag aagtagattc840
atggtggtag agtgtgcctg attgctgggtg gagaaccogt ctttatacct cccgaggatg900
gggagaggag gtgtctgtga ggtgagggtc actgctcctc ccagcacaaa caca 954

```

(2) INFORMATION ON SEQ ID NO. 65:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2213 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

ggcgggacccg ccggggggtcg aggcctgcct ctccgagagc tccctggcgcg gccgtcccg 60
cccggggccc cagggtgcgt tcccctagag agggattttc cgggtctcgtg ggcagaggaa 120
caaccaggaa cttgggggtc agtctccacc ccacagtggg gcggatccgt cccggataag 180
accgctgtc tggccctgag tagggtgtga cctccgcagc cgcagaggag gacgcagcc 240
ggcctcgaag aacttctgct tgggtggctg aactctgac ttgacctaga gtcattggcca 300
tggcaaccaa aggaggtact gtcaaagctg ctccaggatt caatgccatg gaagatgcc 360
agaccctgag gaaggccatg aaagggtctg gcaccgatga agacgccatt attagcgtcc 420
ttgcctaccg caacaccgcc cagcgccagg agatcaggac agcctacaag agcaccatcg 480
gcagggaact gatagacgac ctgaagtcag aactgagtgg caacttcgag cagggtgattg 540
tggggatgat gacgcccacg gtgctgtatg acgtgcaaga gctgcgaagg gccatgaagg 600
gagccggcac tgatgagggc tgcctaattg agatcctggc ctcccggacc cctgaggaga 660
tccggcgcat aagccaaacc taccagcagc aatatggacg gagccttgaa gatgacattc 720
gctctgacac atcgttcatg ttccagcgag tgctgggtgtc tctgtcagct ggtgggaggg 780
atgaaggaaa ttatctggac gatgctctcg tgagacagga tgcccaggag ctgtatgagg 840
ctggagagaa gaaatggggg acagatgagg tgaaatttct aactgttctc tgttcccga 900
accgaaatca cctgttgcat gtgtttgatg aatacaaaag gatatacag aaggatattg 960
aacagagtat taaatctgaa acatctggtg gctttgaaga tgctctgctg gctatagtaa1020
agtgcattag gaacaaatct gcataatttg ctgaaaagct ctataaatcg atgaagggt1080
tgggcaccga tgataacacc ctcatcagag tgatggtttc tcgagcagaa attgacatgt1140
tggatatccg ggcacacttc aagagactct atggaaagtc tctgtactcg ttcatcaagg1200
gtgacacatc tggagactac aggaaagtac tgcttgttct ctgtggagga gatgattaaa1260
ataaaaatcc cagaaggaca ggaggattct caacactttg aattttttta acttcatttt1320
tctacactgc tattatcatt ctgtattatt attcacctat aattagtcat tatgatgctt1440
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taaagctgta cttgcatttc aaagcttata ctttctactt tgtgtttcac agacattgaa1560
aaatatgtat tccatgtttt tttcttttca gtgaaaaatt ttttaaatgg aagactgttc1620
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taagttttcc atgggagact tcttcatca catcttatgt tgaaatcact ttctgtagtc1860
aaagtatacc aaaaccaatt tatctgaact aaattctaaa gtatgggtat acaaaccatal920
tacatctggt taccaaacat aaatgctgaa cattccatat tattatagtt aatgtcttaa1980
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gtaatgctct gaatttagta tgatataaag aaaacttttt tgtgctaaaa atacttttta2100
aaatcaattt tgttgattgt agtaatttct atttgcactg tgcttttcaa ctccagaaac2160
attctgaaga tgtacttgga ttttaattaaa aagttcactt tgtaaaaaaa aaa 2213

```

(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2878 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

cctcgtgcag gtgcacogct tggtcctaaa agctctggag gatggccggg catatgggtc 60
tccatgggtgc aacaaacaga tcacaagggtg cctaattgaa tgcgagatg aatataaata 120
taatgtggag gctgtggagc tgctaattcg caatcatttg gttaatatgc agcagtatga 180
tcttcaccta gcgcagtcac tggagaatgg cttaaactac atggctgtgg catttgctat 240
gcagttagta aaaatcctgc tgggtgatga aaggagtgtt gctcatgtta ctgaggcaga 300
tctgtccac accattgaaa cctcatgag gattaatgct cattccagag gcaatgctcc 360
agaaggattg cccagctga tggaaagtag gcgatccaac tatgaagcaa tgattgatcg 420
tgctcatgga ggcccaaaact ttatgatgca ttctgggac tctcaagcct cagagtatga 480
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ccattcagca gcagctggcc gcgacagtac caaagcttct tctgcatttg ttggacagat 600
gcaccagcaa ggaatactga agaccgatga tctcataaca aggttcttct gtctgtgtac 660
tgaaatgtgt gttgaaatca gttaccgtgc tcaggctgag cagcagcaca atcctgctgc 720
caatcccacc atgatccgag ccaagtgtca tcacaacctg gatgccttgc ttcgactcat 780
tgactgtctc gtgaaacact caggggaggc caccaacact gtcacaaaga ttaatctgct 840
gaaacaggtc cttggtatag tagtgggagt tctccttcag gatcatgatg ttcgtcagag 900
tgaatttcag caacttccct accatcgaat ttttatcatg cttctcttgg aactcaatgc 960
acctgagcat gtgttgaaa ccattaattt ccagacactt acagcttctc gcaatacatt 1020
ccacatcttg aggcctacca aagctcctgg ctttgtatat gcctggcttg aactgatttc 1080
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gtatgcacag ctactgattg atttattcaa atatttagcg ccttccctta gaaatgtgga 1200
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gcattgttc ccagagttcc tttgtgatta ccattatggg tctgtgatg tgatcccacc 1320
taattgtatc cagttaagaa atttgatcct gagtgccttt ccaagaaaca tgaggctccc 1380
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cactgtgccc cagaaatcga aaagtatttc cagtccgtcg cacagtgtg catgggacag 2040
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tgtacgtgtc agtctagagg tctcactgca ccgagttcat aaactgactg aagaatcct 2160
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catgtctctt gacattcctg gtgtcccaaa gaatagcaaa aagccagttt gaattatgt 2520
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agtcttccat ttgtctctac ccaaacgtat tccaaagctg actgcatttg taccatctta 2700
tttcttttgg ggattataca cctcagccgc ctgagatggg ggtcagctct ttatataaag 2760
ggaaaccaga ccaggcctaa agcccacccc ctaccctcac cccccacac atcctctct 2820
gaaactttta aaaccagtgg ggatttttag gaaagggaac ccaaaccgcg attaatgt 2878

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(2) INFORMATION ON SEQ ID NO. 68:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 701 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

atgatatttt ggatgtagtc ttttgattgt ttaaattctta aaaagtaatg ggatcttttg 60
acactggggt atgttttatt tttatgtgtg caaattttta ccatattctt ttctagttaa120
agaggaaaaa gcaagttgct ccagaaaaac ctgtaaagaa acaaaagaca ggtgagactt180
cgagagccct gtcattcttc aaacagagca gcagcagcag agatgataac atgtttcaga240
ttgggaaaaat gaggtacgtt agtgttcgcg attttaaagg caaagtgcga attgatatta300
gagaatattg gatggatcct gaaggtgaaa tgaaaccagg aagaaaagggt atttctttta360
atccagaaca atggagccag ctgaaggaac agatttctga cattgatgat gcagtaagaa420
aactgtaaaa ttcgagccat ataaataaaa cctgtactgt tctagtgtt ttaatctgtc480
tttttacatt ggcttttgtt ttctaaatgt tctccaagct attgtatgtt tggattgcag540
aagaatttgt aagatgaata ctttttttta atgtgcatta ttaaaaaatat tgagtgaagc600
taattgtcaa ctttattaag gattactttg tctgccacc acctagtgtg aaataaaatc660
aagtaataca atcttaaaaa aaaaaaaaaa aaaagtcgag c 701

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(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 817 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

gttttttttt tttttttttt ttttttttaa gcacagaaaag cttttattac cacagaggaa 60
atcaggaaat gctggaggca gcctcgtag ctgtgtgatc agggagggga cagcaggcgg120
gaaccctgtca tcaatcatgt ctgggcagtc tcccaaccaa caggtttggt tggttcaggal80
gaggcttttg ctgggctgtg tgtgtgtatg atcaggaagg tcagcctcaa caaatgggct240
tcttcctgga cataggacag ccagaatcgg ggacaccagc tgcacagaca ccaccttaaa300
atggaaatca aattagggtc attacatcag gaagtacatt tcaccctgat cataaaagag360
ggacaaggga gcactgggct ctactggata gcctttcttt tagataagat gcttttaaaa420
gttaaacatt ggcagggcct ttcccctagc taacagcaag cagcacacaa ttccaagtca480
gcttgtaaaag cttttgttat ctttgttatc tgttattatt tggattttga acgaaattga540
tggagtacga gccggttagag gaatcctggt tgatctggaa attttccgtg gagagcccaa600
aaggctcgga aaccaagttc ccaagatctt ttaatttacc taacatctct tcttttagtc660
tttcattacg ttcttcaatt tgcttaggta atctcataca agcttctctt gcttgatgta720
ttgatgaagg ttcccgcctg ctgtcccctc cctgatcaca cagctaacga ggctcctcca780
gcatttcctg atttcctctg tggtaataaa agctttc 817

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(2) INFORMATION ON SEQ ID NO. 70:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2686 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

gcaaggccta ctgtcggtcg ggaggggagg tgtagccggt ctttgggggt aggcggtagt 60
ggcggaagag gttcgggcggc tgatggcgga tcaggatcgg aagcctgcgt aactttctcc 120
cttgatccgg gaggctttcc actggattca caatgacatc ctttcaagaa gtccatttgc 180
agactttcaa ctttgcccat gtcatctttc aaaatgtggc caagagttac cttcctaattg 240
cacacctgga atgtcattac accttaactc catatattca tccacatcca aaagattggg 300
ttggtatatt caaggttggg tggagtactg ctctgtgatta ttacacgttt ttatgggtccc 360
ctatgcctga acattatgtg gaaggatcaa cagtcaattg tgtactagca ttccaaggat 420
attaccttcc aaatgatgat ggagaatttt atcagttctg ttacgttacc cataagggtg 480
aaattcgtgg agcaagtaca cctttccagt ttcgagcttc ttctccagtt gaagagctgc 540
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ttgagttgaa aattgagaaa accatgaaaag aaaaagaaga actgttaaaag ttaattgccc 660
ttctggaaaa agaaaacagca caacttcgag aacaagttgg gagaatggaa agagaactta 720
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cacaaagctt aaaaatggaa aatgaagagt ttaagaagag gttcagtgat gctacatcca 840
aagcccatca gcttgaggaa gatatttgtt cagtaacaca taaagcaatt gaaaaagaaa 900
ccgaattaga cagtttaaaag gacaaaactc agaaggcaca acatgaaaga gaacaacttg 960
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gtttttttaa ggagcaactt cgtaaaagcag aggaacaggt tcaggcaact cggcaagaag 1260
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acctgcatac tgcacgcttg gaaaacgaga aagtgaaaaa gcagttagct gatgcagtg 1380
cagaacttaa actaaatgct atgaaaaaag atcaggacaa gactgataca ctggaacacg 1440
aactaagaag agaagttgaa gatctgaaac tccgtcttca gatggctgca gaccattata 1500
aagaaaaatt taaggaatgc caaaggctcc aaaaacaaat aaacaaaact tcagatcaat 1560
cagctaataa taataatgtc ttcacaaaga aaacggggaa tcagcagaaa gtgaatgat 1620
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caaaatgcaa taaatatgct gatgaacttg caaaaatgga gctgaaatgg aaagaacaag 1860
tgaaaaattg tgaaaaatgt aaacttgaac tagctgaagt acaggacaat tataaagaac 1920
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tagaccactg aggagaccat agagcggatg ctttcatgca ccctttactg cactttctga 2520
ccaggagcta ctttgagttt ggtgttacta ggatcagggt cagtctttgg cttatcaata 2580
aattttaatc tctgttaatc ttacaaaaat ttaaaaaaaa aaaaaaaat cgtactttat 2640
ttatccctag ttgcagactg ctgaataaag gtcaaggatt atccat 2686

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(2) INFORMATION ON SEQ ID NO. 72:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 922 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

ctgctctgaa aagccatctt tgcattgttc ctcacccgcc tccttgctcg cggcagccgc 60
ctccgcgcgc cgcctcctcc gccgcgcgcg actccggcag ctttatcgcc agagtccctg120
aactctcgct ttctttttta tcccttgcac cggatcaccg gcgtgcccc aatgtcaga180
cgcagccgta gacaccagct ccgaaatcac caccaaggac ttaaaggaga agaaggaagt240
tgtggaagag gcagaaaatg gaagagacgc ccctgctaac gggaatgcta atgaggaaaa300
tggggagcag gaggctgaca atgaggtaga cgaagaagag gaagaagggg ggtgatggtg360
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gtgggcagtg ccacccgcag atgacacgcg ctctccacca cccaacccaa accatgagaa660
tttgcaacag gggagggaag aaggaccaaa acttccaagg ccctgctttt tttcttaaaa720
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tgttaggggt caaccatttt taatgatctc ggatgaccaa accagccttc ggaagcgttc840
tctggcctac ttctggactt ttacgttggg gggttgttga ccatgttcaa ttataatccc900
aaaaggggga aaaaaaacct tt

```

922

(2) INFORMATION ON SEQ ID NO. 73:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 870 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ggaagtggcg gtgcgagggc tgctgcacag cgagcggagc cgcgggtccg acggcagcgc 60
gtgccccgag ctctccgcct ccccccgccc gccagccgag gcagctcgag cccagtcgcg 120
ggccccagca gcagcgccga gagcagcccc agtagcagcg ccattggcgg gtggaacgcc 180
tacatcgaca acctcatggc ggacgggacc tgtcaggacg cggccatcgt gggctacaag 240
gactcgccct ccgtctgggc cgcggtcccc gggaaaaacgt tcgtcaacat cacgccagct 300
gaggtgggtg tcttggttg caaagaccgg tcaagttttt acgtgaatgg gctgacactt 360
ggggggccaga aatgttcggt gatccgggac tcaactgctgc aggatgggga atttagcatg 420
gatcttcgta ccaagagcac cggtgggggc cccaccttca atgtcactgt caccaagact 480
gacaagacgc tagtcttct gatgggcaaa gaaggtgtcc acggtgggtt gatcaacaag 540
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ccccctcacc gctccccaca gctttgcacc cctttctctc ccatacacac acaaaccatt 660
ttattttttg ggccattacc ccataccctt tattgctgcc aaaaccacat gggctggggg 720
ccagggctgg atggacagac acctccccct acccatatcc ctcccgtgtg tggttggaaa 780
acttttgttt tttggggttt tttttttctg aataaaaaag attctactta aaaaaaaaaa 840
aaaaaaaaaa aaaaaaaaaa aaaggggggg

```

(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1418 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

ataaaagagg aaagagtgcc caggtcttca ctccactgcg actgcagaac tcagagctgc 60
tcttcctctg tggccagtgg gggaccagca tcatgaagtg gatggtggtg gtcttgggtct 120
gcctccagct cttggaggca gcagtgggtca aagtggccct gaagaaattt aagtctatcc 180

gtgagaccat gaaggagaag ggcttgcctgg gggagtccct gaggaccac aagtatgatc 240
ctgcttggaa gtaccgcttt ggtgacctca gcgtgacctc cgagcccatg gcctacatgg 300
atgctgccta ctttgggtgag atcagcatcg ggactccacc ccagaacttc ctggctcttt 360
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ccagtcactc ccgcttcaac cccagcgagt cgtccacctc ctccaccaat gggcagacct 480
tctccctgca gtatggcagt ggcagcctca cgggcttctt tggtatgac accctgactg 540
tccagagcat ccaggtcccc aaccaggagt tgggcttgag tgagaatgag cctggtagca 600
acttcgtcta tgcgcagttt gatggcatca tgggcttggc ctacctgct ctgtccgtgg 660
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cctactattc cgtctacgac ttgggcaaca acagagtagg ctttgccact gccgcctaga 1260
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tgtatctgtc tttccactct ggattcagcc ttcttttctt ggactctgga ctttctctaa 1380
taataaatag ttcttctttt aaaaaaaaaa aaaaaaaaaa 1418

```

(2) INFORMATION ON SEQ ID NO. 76:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1712 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

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gtggcagaaa acctcatgac acaatctctc cgcctccctg tgttggtgga ggatgtctgc 60
agcagcattt aaattctggg agggcttggg tgtcagcagc agcaggaggg gcagagcaca 120
gcacgcgtcg gaccagactc gtctcaggcc agttgcagcc ttctcagcca aacgccgacc 180
aaggaaaact cactaccatg agaattgcag tgatttgctt ttgcctccta ggcatcacct 240
gtgccatacc agttaaacag gctgattctg gaagttctga ggaaaagcag ctttacaaca 300
aatacccaga tgctgtggcc acatggctaa accctgaccc atctcagaag cagaatctcc 360
tagccccaca gaatgctgtg tcctctgaag aaaccaatga ctttaaaca gagacccttc 420
caagtraagtc caacgaaagc catgaccaca tggatgatat ggatgatgaa gatgatgacg 480
accatgtgga cagccaggac tccattgact cgaacgactc tgatgatgta gatgacactg 540
atgattctca ccagtctgat gagtctcacc attctgatga atctgatgaa ctggtcactg 600

atcttccac ggacctgcca gcaaccgaag ttttcactcc agttgtcccc acagtagaca 660
catatgatgg ccgagggtgat agtggtggtt atggactgag gtcaaaatct aagaagtttc 720
gcagacctga catccagtac cctgatgcta cagacgagga catcacctca cacatggaaa 780
gcgaggagtt gaatggtgca tacaaggcca tccccgttgc ccaggacctg aacgcgcctt 840
ctgattggga cagccgtggg aaggacagtt atgaaacgag tcagctggat gaccagagtg 900
ctgaaaacca cagccacaag cagtccagat tataaagcg gaaagccaat gatgagaca 960
atgagcattc cgatgtgatt gatagtcagg aactttccaa agtcagccgt gaattccaca 1020
gccatgaatt tcacagccat gaagatatgc tgggtgtaga ccccaaaagt aaggaagaag 1080
ataaacacct gaaatttctg atttctcatg aattagatag tgcattctct gaggtcaatt 1140
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gcaaaatgaa agagaacatg aaatgcttct ttctcagttt attggttgaa tgtgtatcta 1260
tttgagtctg gaaataacta atgtgtttga taattagttt agtttggtgg ttcattgaaa 1320
ctccctgtaa actaaaagct tcagggttat gtctatgttc attctataga agaaatgcaa 1380
actatcactg tattttaata ttgttatct tctcatgaat agaaatttat gtagaagcaa 1440
acaaaatact ttaccact taaaaagaga atataacatt ttatgtcact ataattcttt 1500
gttttttaag ttagtgata tttgttgtg attatctttt tgtggtgtga ataaatcttt 1560
tatcttgaat gtaataagaa ttggtgtgt tcaattgctt attgttttc ccacggttgt 1620
ccagcaatta ataaaacata accttttta ctgcctaaaa aaaaaaaga gaaaagaaaa 1680
aaaaagaaaag aaaaaaaggg gagggagggg ag
1712

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(2) INFORMATION ON SEQ ID NO. 78:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(A) LIBRARY: cDNA library

| | | | | | | |
|-------------|-------------|------------|-------------|------------|-------------|------|
| accgcccccg | ctgtgggtct | cagcagctcg | ggcgccggga | ggggtggcag | cggcaaggca | 60 |
| gccagtttc | gcgaaggctg | tgggcgcgc | gcggcccgca | ggcaccggc | acgcgccttc | 120 |
| cccgaggca | cccggcacgc | gccttccccg | ccgccacgat | gcccaagagg | aaggtcagct | 180 |
| ccgcccgaag | gccgccaaag | aagagcccaa | gaggagatcg | gcgcggttct | cagctaaacc | 240 |
| tcttgcaaaa | gtggaagcga | accgaaaaag | gcagcagcga | aggataaatc | ttcagacaaa | 300 |
| aaagtgcaaa | caaaaaggaa | aaggggagca | aagggaaaaac | aggccgaagt | ggctaaaccaa | 360 |
| gaaactaaa | aagacttacc | tgcggaaaac | ggggaaaacga | agactgagga | gagtccagcc | 420 |
| tctgatgaag | caggagagaa | agaagccaag | tctgattaat | aaccatatac | catgtcttat | 480 |
| cagtggctcc | tgtctccctt | cttgtagaat | ccagaggaat | atttttatca | actattttgt | 540 |
| aaatgcaagt | tttttagtag | ctctagaaac | atttttaaga | aggagggaat | cccactcat | 600 |
| cccatttttt | aagtgtaaat | gctttttttt | aagaggtgaa | atcatttgtc | ggtgttttat | 660 |
| tttttggtag | aaccagaaaa | tagtgtggga | tattgaatta | tgggaggctc | tgactgtctc | 720 |
| gggtgtcagc | ttaacattcc | acagatgggg | ggttagtttt | tatatcctat | aatacaaaagc | 780 |
| ctattaaatg | gcaatcatgga | gtcagtcctg | catttaaatgt | cttgaacatt | ttaaattact | 840 |
| ctctattacca | tgttgttttt | tagtagaatt | gttttctaaa | gaaaaccact | ctttgatcat | 900 |
| ggtctctctc | gccagaattg | tgtgcactct | gtaacatctt | tgtgttagtc | ctgttttctc | 960 |
| ataaactctg | ttaactgtgt | gtgaaagatt | acagatttga | acatgtagt | tacgtgctgt | 1020 |
| ctgagttgtga | actggtgggc | cgtatgtaac | agctgaccaa | cgtgaagata | ctggtacttg | 1080 |
| atagcctctt | aaggaaaatt | tgcttccaaa | ttttaagctg | gaaagtcact | ggaataaact | 1140 |
| taaaaaagaa | ttacaataca | tggcttttta | gaatttcgtt | acgtatgtta | agatttgtgt | 1200 |
| acaaaattgaa | atgtctgtac | tgatcctcaa | ccaataaaat | ctcagttatg | aaaaataaaa | 1260 |
| aaaaaaaaaa | aaa | | | | | 1273 |

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2342 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

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ccctggacca ccggactggc ctggggcggg acgtggggcg gggggcgcg cgtgcggcac 60
gctgcaggcg tgaagcggcg gcggcggtgg ggactgcacg tagcccggcg ctcggcatgg 120
ctctcctggt gctcgggtctg gtgagctgta ccttctttct ggcatgaaat ggtctgtatt 180
cctctagtga tgatgtgac gaattaactc catcaaattt caaccgagaa gttattcaga 240
gtgatagttt gtggcttgta gaattctatg ctccatgggtg tggtcactgt caaagattaa 300
caccagaatg gaagaaagca gcaactgcat taaaagatgt tgtcaaagtt ggtgcagttg 360
atgcagataa gcatcattcc ctaggaggtc agtatgggtg tcagggattt cctaccatta 420
agatttttgg atccaacaaa aacagaccag aagattacca aggtggcaga actggtgaag 480
ccattgtaga tgctgcgctg agtgctctgc gccagctcgt gaaggatcgc ctcgggggac 540
gaagcggagg atacagttct ggaaaacaag gcagaagtga tagttcaagt aagaaggatg 600
tgattgagct gacagacgac agctttgata agaattgtct ggacagtga gattttgga 660
tggttgagtt ctatgctcct tgggtgggac actgcaaaaa cctagagcca gagggtgctg 720
ccgcagcttc agaagtaaaa gagcagacga aaggaaaagt gaaactggca gctgtggatg 780
ctacagtcaa tcagggttctg gcctcccgat acgggattag aggatttctt acaatcaaga 840
tatttcagaa aggcgagttc cctgtggatt atgacggtgg gcggacaaga tccgacatcg 900
tgtcccgggc ccttgatttg tttctgata acgccccacc tctgagctg cttgagatta 960
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tgccccatat ccttgatact ggagctgcag gcagaaattc ttatctggaa gttcttctga 1080
agttggcaga caaatacaaa aagaaaatgt gggggtggct gtggacagaa gctggagccc 1140
agtctgaact tgagaccgcg ttggggattg gaggggttgg gtaccccgcc atggccgccal 1200

tcaatgcacg caagatgaaa tttgctctgc taaaaggctc cttcagtga caaggcatcal 1260
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gtgaaggggac attctctaca ctacagatgac tctaccagtg gccttttaac caagaagtag 1560
tacttgattg gtcatttgaa aacactgcaa cagtgaactt ttgcatctca agaaaacatt 1620
gaaaaattct atgaattgtt gtagccgggtg aattgagtcg tattctgtca cataatattt 1680
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gtctttctct cccacaaaact tttttaaaac aaaaaacaag cctcttttct ttagatgggt 1980
ccacctatgc ccaccacaac agagatttta catggaaacc gggctcagtg agaactgatt 2040
tctgcccaca tatttgcctt tgggctgtct ctagtacta attattaagg aatctagctg 2100
gttatcacgt tcaaggcttt ctatgttgtt aatgaacctc aaaatagccg ttaagacatg 2160
aaatacacga gcagggtacc aatgogaaca ggtagtccgc atttatgtaa aacattcaga 2220
aaatgaagtt ttgaatttgt tggaaacattc aaaggacttg agagcatttt attgtaactt 2280
aaaaaaaaaa atacaactgt cactaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2340
aa
2342

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(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1959 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

gcagttatat aataagtttg ggagacaaaa tgatacgcac acgagagaag atgaagaaga 60
 tactcaaaagt tccaaatctg aagaacatca tttgtactct aatccaatca aagaagaaat 120
 gactgagctt aagttctcta agtactctga aatgagtgag gaaaaacgag ccaaactctg 180
 tgaaattgag ctcaaagtta tgaagtttca ggatgaattg gaatctggga aaagacctaa 240
 aaaaccaggc cagagttttc aggagcaagt agaactactac agagataaac ttcttcaacg 300
 agagaaagag aaagagttag aaagagaacg agaaagagac aagaaagata aagaaaaatt 360
 ggaatctcgc tccaaagaca agaaggaaaa agatgagtggt actccgacaa ggagggaaaag 420
 gaagaggcga cacagtacat cccccagccc atctcgcagt agcagtggtg gacgagtgaa 480
 atccccatca ccaaaatcgg agcgatcaga gcgttcagaa agatctcata aagagagctc 540
 acgggtccagg tcattctcaca aagattctcc tagagatggt agcaaaaaag ccaaaagatc 600
 accatctggt tcaaggacac ctaaaagggtc taggcgatca cggtctagat ctcttaaaaa 660

atcaggaaaag aagtcagat cccagtcag atctccacac aggtctcata aaaagtcaaa 720
 gaaaaacaaa cactgacgta aatttttaag atgctgtcac ttattggaaa tgcgatttgt 780
 tttgtgcctg aacgggtctgt tttttaaaaa aacaaaaaat caaatgaaag agcattcctg 840
 ggggtttttg tttgtttgtg tatgcatgtg taaactcatg agcaactgca tctgtagatc 900
 tgtcattgtt ttatattgtg taaattactt tcattgtggc tatttctcaa gatgaaattt 960
 ttattgttct aatggatttc atcagaaatg tgtataatgg atctgctgac agtagtagta 1020
 ttttgtttta ggatgtttgt acctagcaaa aataatacag atgtcttccc ccttttgtal 1080
 gctttgacaa tttgaattag atttcaaata aaatctgaac agaaaactat aatgttgttt 1140
 ttttgcccca ccggtgatat taagtccctt aaagtcctac tgagtttcac actactgttg 1200
 tgcttcttat acctgatgca ctttataagc cccagtggtc aagtagctta agttttatat 1260
 ttactaagat gactatccaa attaagggac ctgagactcc tatttggtgg tttgctaacc 1320
 atttgctttt gataagtttc tcttgggtta tactaatacc cagatatcaa agactaggta 1380
 gatatggcat ggcgttttgt tagtggaatg cctggctaaa acattttttt cacagaagca 1440
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 aaatatcttt tcatttcttc ttctattatg aaagaagttt atttgtaaaa caaattttct 1560
 aacaaggttt ggccatagaa ttctcttgta tgattgttga ccttttataa tcttctgtag 1620
 gctatctttc aaacactggc atcagaatat tttttataag tttgtgttta aacagcttag 1680
 ttgggtccccc cccctactcc caagagactt ggggttagtt atagctttaa gtaaaattta 1740
 aaaaataaaat gtttttcagg aaacttcgta tctaattggt tgtaaattca aggtgcaaaa 1800
 agttgattta aaccatttgc agagttgaac tctattatga aaataaattt gctacgggat 1860
 gaggaagaaa taaaacttgt gtaatgttgg tcataatact gctataaata taataaaggg 1920
 ttatgtagaa ttgaactgac aaaaaaaaaa aaaaaaaaaa 1959

(2) INFORMATION ON SEQ ID NO. 81:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3708 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

gccccatttta tcacgcacgg tagacaagct tttttttttt ttttttttta cagcttataa 60
 cacaactttt attagaaaaa ttatacataa catagcatca actattttta agaacaatat 120
 taaacccgat aagcaacaaa aaccagacta acaaaatgtg taacaagaaa ctaatgacct 180
 ttctaaaatc aaacattcaa ttatctacaa tgtcttttta caaacgggga aaactccttg 240
 gtttacaggc acatcatatt gaatataaag ctgcaatagc aatttttatac aattaccact 300
 ctgaagaaac tgaatcatta aaacagtaat tacgagttca caaattttaaa acattttcaca 360
 taattttaaa ttattgggta tacactgaag tctgagtttc aaaagtgtatt tttttttccc 420
 acaaaagtgt caacacttaa gctagaactt tcagtgttaa ctttgcccta aaaagttaag 480
 acatattctg ataatacataa cagtcacatg atttctgatg ctatctgggc tgtaataaat 540

aaagtcttta tttggatgta tttttcttca attaaattac aggaaaactgg atataggatt 600
 tgggtgcaac gctattaaag ttccaaacca ggagtgtgca gcaactggaaa aggagatcag 660
 tactaaaact tacaataaat atcagagaag ccgttagttt ttacagcatc gtctgcttaa 720
 aagctaagtt gaccaggtgc ataattttccc atcagctgtt ccttgtagta ggcaggggca 780
 tttctgtttt catgatcgga atactcaa atatccaaac atctttttta acctttgtat 840
 tatagctcct agaaagtatt gttttttaat agtcactcta ctctaatacag gcctagcttt 900
 gctcattttg gagcctcact aaaataacag atttcagtat agccaagtgc atcagaaaaga 960
 ctcaaatgga atgatttaca aaatagaaca ctttaaacca ggtcagtcct atctttttgt 1020
 agctgaaggc tatcagtcac aacacaattt cgcgtacacc tctgctcatt atggaattac 1080
 acttaaaacg aatctcaaga ggggtgacct tgtgttttca gataccatcc ctaaggagag 1140
 tgggttaacag gaagattgcc agtgttactg attgaaagaa gtgtttgttt gtttttttt 1200
 cttgtcaaaag acttacacca tagtttttaa ttaaaactgtc aggcattttt tcagacaggt 1260
 tttccttttc aatgcagtaa tgaagaacta agataaaaaat catgactttt gactgccact 1320
 caacattatt acatgcacca atattgcaca catctgttct gaactgttaa aatcatcttc 1380
 tgagtctctg ggggtgctgt ttctccatca gaacacaaac acaaccatc taatcagttt 1440
 ccttcaaaag tgaatttgac aaatttaatt tactggaaaa aaatgaagaa ggaaaaaggc 1500
 aaagactttg tacagacaaa aatctaagtt ttctcaaaag gttctgtgtc cctacacat 1560
 gggggcaatt tgtaagcact agtgaatcaa acactagcta taatgcttct agctccttat 1620
 ataatatgga accttgggtc aggtgttgct atgatgtcac tgtacgggtc ttctgtgtc 1680
 agctcaatag cttgtctgtt ttaagaacc aagaagctgt agaactttgc ggcagcttgt 1740
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 gtttgttctg ctggcctcca tcaactgactc ctggaggcgg ctgtgctctt caataatggg 2160
 ctcactgata acatcacgct gctgatgctg ctgttgctgg tctctctag gaacctctgg 2220
 tattttcaaat tctttgagga attcatccaa attatctgcc tctctctctt tctctctt 2280
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 tcatgtgcag gctgctctgg caacatcacc cctgctcag agagggcagg gggatcatca 2760
 aagataccgc catcattatt actaataagt ttgtcatcta atattccacc atcatttctc 2820
 tctccaaaat tatcatctt atattgatct tcatattcta aatggttaat ttctcattc 2880
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 atgtcgtcat cctcaaaagc actgccttct ctcatctatc cagcatcctc cattccaaaa 3000
 tcacaaaaat cattttcttg taaaatactg atgttcccaa cttcttctct catggttatc 3060
 tcttccactc tactctgatt caagctgaac tgctgggcca catcgatgtc atctaagtca 3120
 ggcagtggtc gatcaaagtc atgaaattct tcaggtaaag taatggcatt ataagctgtc 3180
 tcccgatctt cctcaggcag gtcaaccaca cctgcccga aagccatctt tatcttaatg 3240
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 cccagtaaga gatgtcctga tgtccgtaat gccattttta cctttgggtga gatgatactc 3360
 ttccacgctg ctctctaaat tacactogaa cacatgggct ttggttagct tcttatccca 3420
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(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3045 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

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gtccattgcc caaaatccgc tatgaaagct tgaccaatcc ccagtaaatt agacctctgg 60
gaaaagagct gccatattac ccatacccca aacaaccaag atcgaactct cactattgtg 120
gatactggaa ttggaatgac caaggctgac ttgatcaata accttggtac tatcgccaag 180
tctgggacca aagcgttcat ggaagctttg caggctggtg cagatatctc tatgattggc 240
cagttcgggtg ttggttttta ttctgcttat ttggttgctg agaaagtaac tgtgatcacc 300
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gacaagaaga agaagaagaa gattaaggaa aagtacatcg atcaagaaga gctcaacaaa 720
acaaagccca tctggaccag aaatcccgac gatattacta atgaggagta cggagaattc 780
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ggacagttgg aattcagagc ccttctattt gtcccacgac gtgctccttt tgatctgttt 900
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ctgtagttga caattctgca tgtactagtc ctctagaaat aggtttaaact gaagcaactt2520
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gttaaaaagat attgtgtgac agtgtcttat ttagggggaa aggggagtat ctggatgaca2760
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caagggttga catggtcttc ccagcatgta ctcagcaggt gtgggggtga gcacatgtag2880
gcacagaaaa caggaatgca gacaacatgc atccctgcg tccatgagtt acatgtgttc2940
tcttagtgct cacgttggtt tgatgttatt catggaatac cttctgtgct aaatacagtc3000
acttaattcc ttggccaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa

```

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

cagtggcggc gcaaccagcc ttctagggcg gcgaggaggt ggagtcaaca tatcaatgga 60
gcaagtcaca gtcgtcgatg ccagcttctt cttgaaatct acccagaatg gaatcctgac 120
aatgatacag gacacacaat gggatgatcca ttcatgttgc agcagtctac aaatccagca 180
ccaggaattc tgggacctcc acctccctca ttcatcttg ggggaccagc agttggacca 240
agaggaaatc tgggtgctgg aaatggaaac ctgcaaggac ctagacacat gcagaaaggc 300
agagtggaaa ctagcagagt tgttcacatc atggattttc aacgagggaa aaacttgaga 360
taccagctat tacagctggt tgaatggca accacagagg atgctcaggc cgagtggaat 480
aaaattaatg aggcatttat tgaaatggca accacagagg atgctcaggc cgagtggaat 480
tattacacaa ccacaccagc gttagtattt ggcaagccag tgagagttca tttatcccag 540
aagtataaaa gaataaagaa acctgaaggga aagccagatc agaagtttga tcaaaagcaa 600
gagcttggac gtgtgataca tctcagcaat ttgccgcatt ctggctattc tgatagtgtc 660
gttctcaagc ttgctgagcc ttatgggaaa ataaagaatt acatattgat gaggatgaaa 720
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gaatgttaac caaaaaaaaaa aacagttgtg gtttttatcc gctcttaaac tttgtgcatg 2760
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(2) INFORMATION ON SEQ ID NO. 84:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3462 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

ctggatcgta caagaaggga gacaaggacc actgacaaga taaggcctag caggaaacga 60
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 cccgcccgga agaagcgacc aaagcgctg aggaccggca acatggtgcg gtcggggaat 180

aaggcagctg ttgtgctgtg tatggacgtg ggttttacca tgagtaactc cattcctggg 240
 atagaatccc catttgaaca agcaaagaag gtgataacca tgtttgtaca gcgacaggtg 300
 ttgtctgaga acaaggatga gattgcttta gtctctgttg gtacagatgg cactgacaat 360
 cccctttctg gtggggatca gtatcagaac atcacagtgc acagacatct gatgctacca 420
 gattttgatt tgctggagga cattgaaagc aaaatccaac caggttctca acaggctgac 480
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 ttgtgagaaga ggcatattga aatattcact gacctcagca gccgattcag caaaagtgcag 600
 ctggatatta taattcatag ctggaagaaa tgtgacatct ccctgcaatt ctctctgctt 660
 ttctcacttg gcaaggaaga tggaaagtggg gacagaggag atggccctt tcgcttaggt 720
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 gatgaggaac aaatgaaata taaatcggag gggaaagtgt tctctgtttt gggattttgt 1200
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 tctcattctt tgccctgagt tccagttcct ctttggtgta cagacttctt ggtaccaggt 3360
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 ttaaaggcat aaatgactca aaaaaaaaaa aaaaaaaaaa aa 3462

(2) INFORMATION ON SEQ ID NO. 85:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 668 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

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atagggccgg tgctgcctgc ggaagccggc ggctgagagg cagcgaactc atctttgcc 60
gtacaggagc tcgtgccgtg gcccacagcc cacagcccac agccatgggc tgggacctga 120
cggtgaagat gctggcgggc aacgaattcc aggtgtccct gagcagctcc atgtcgggtg 180
cagagctgaa ggcgcagatc acccagaaga tcggcgtgca cgccttcag cagcgtctgg 240
ctgtccaccc gagcgggtgtg gcgctgcagg acagggtccc ccttgccagc cagggcctgg 300
gccccggcag cacggctcctg ctggtgggtgg acaaatgcga cgaacctctg agcatcctgg 360
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acctgaagca gcaagtgagc gggctggagg gtgtgcagga cgacctgttc tggctgacct 480
tcgaggggaa gccctggag gaccagctcc cgctggggga gtacggcctc aagcccctga 540
gcaccgtgtt catgaatctg cgcctgcggg gaggcggcac agagcctggc gggcggagct 600
aagggcctcc accagcatcc gagcaggatc aagggccgga aataaaggct gttgtaaa 660
gaaaaaaa

```

(2) INFORMATION ON SEQ ID NO. 86:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 671 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

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agtggaggag ggagagacgc tggcccggga cccgaggggc gtgggcatcg ggaggcgggc 60
ccgggttagg ggcgggaccg ccgcctgggt aaaggcgctt atttcccagg cagccgctgc 120
agtcgccaca cctttgcccc tgetgcgatg accctgtcgc cacttctgct tcggacgtcc 180
ccacggcggc ggtgcaggcg tcccctctgc aagcgttaga cttctttggg aatgggccac 240
cagttaacta caagacaggc aatctatacc tgcggggggc cctgaagaag tccaatgcac 300
cgcttgctaa tgtgaccctc tactatgaag cactgtgcgg tggctgccga gccttctga 360
tccgggagct cttcccaaca tggctgttgg tcatggagat cctcaatgtc acgctgggtg 420
cctacggaaa cgcacaggaa caaaatgtca gtggcagggtg ggagttcaag tgccagcatg 480
gagaagagga gtgcaaattc aacaagggtg aggcctgcgt gttggatgaa cttgacatgg 540
agctagcctt cctgaccatt gtctgcatgg aagagtttga ggacatggag agaagtctgc 600
cactatgcct gcagctctac gccccagggc tgtcgccaga cactatcatg gagtgtgcaa 660
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ccccaaaaaa aaaaccgcgt cggtcgac 1108

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(2) INFORMATION ON SEQ ID NO. 89:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 720 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

aaagcagccg cggcgccgg gtgcctcaca gcacgctgcc acgccgacgc agacccctct 60
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cgccctgggg acagcaaagg ctttgatgaa tacatgaagg agctaggagt gggaatagct180
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gaaaaagtag aataaaaaatt ccatacatcac ttggacagg agttaattaa gagaatgacc540
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taggatcacc cctttggtta ataaataaat gtgtttgtgc taaaaaaaaa aaaaaaaaaa720

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(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 837 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

ctctcgcgag gattggctgt tagcggcggt gtagttaagc tcgtgtaacg gcggcggtgt 60
cggcagctgc tgtagcgaag agagtttggc gcgatgtctc acaccatttt gctggtacag120
cctaccaaga ggccagaagg cagaacttat gctgactacg aatctgtgaa tgaatgcatg180
gaagggtgtt gtaaaatgta tgaagaacat ctgaaaagaa tgaatcccaa cagtcctct240
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cactgggggg gttgggggtg gcttggaaca caggtgtgta cagcgtgctg tagtggaagt480
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aagtccttgg aaaaaataat aaatgtcctt tagttataaa aaaaaaaaaa aaaaaaa 837

```

(2) INFORMATION ON SEQ ID NO. 91:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 498 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

gtagggtcag cgtcggaggc ggtagtgcag gtggcggttc cttgagggaag agtgagggtt 60
ccaaacttttc tgcttatctg ggaggtgttg ggcgcggaca gtcgagatgt cagagaaaaa120
gcagccggta gacttaggtc tgtagagga agacgacgag ttggaagagt tccctgccga180
agactgggct ggcttagatg aagatgaaga tgcacatgtc tgggaggata attgggatga240
tgacaatgta gaggatgact tctctaata gttacgagct gaactagaga aacatgggta300
taagatggag acttcatagc atccagaaga agtgttgaag taacctaaac ttgacctgct360
taatacattc tagggcagag aaccaggat gggacactaa aaaaatgtgt ttatttcatt420
atctgcttgg atttatttgt gtttttgtaa cacaaaaaat aaatgttttg atataaaaag480
gaaagagaaa aattgcgg                                     498

```

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cggctcgagc tgggtacaaca gggcacacgt gtttcacgtt gacagggttg cttggggacgc 60
tagtaaccat gggcttgctg acttagccaa agaagagtta agaagaaaat acacacaagt 120
atacagactg ttcttagttt cttagactta tctgcatatt ggataaaaata aatgcaattg 180
tgctcttcat ttaggatgct ttcattgtct ttaagatgtg ttaggaatgt caacagagca 240
aggagaaaaa aggcagtcct ggaatcacat tcttagcaca cctacacctc ttgaaaatag 300
aacaacttgc agaattgaga gtgattcctt tcctaaaagt gtaagaaagc atagagattt 360
gttcgtattt agaatgggat cacgaggaaa agagaaggaa agtgattttt ttccacaaga 420
tctgtaatgt tattttccact tataaaggaa ataaaaaatg aaaaacatta tttggatata 480
aaaagcaaat aaaaacccaa ttcagtctct tctaagcaaa attgctaaag agagatgaac 540
cacattataa agtaatcttt ggctgtaagg cattttcatc tttccttcgg gttggcaaaa 600
tattttaaag gtaaaacatg ctggtgaacc aggggtgttg atggtgataa gggaggaata 660
tagaatgaaa gactgaatct tcctttgttg cacaaataga gtttgaaaaa agcctgtgaa 720
aggtgtcttc tttgacttaa tgtctttaa agtatccaga gatactacaa tattaacata 780
agaaaagatt atatattatt tctgaatcga gatgtccata gtcaaatttg taaatcttat 840
tcttttgtaa tatttattta tatttattta tgacagttaa cattctgatt ttacatgtaa 900
aacaagaaaa gttgaagaag atatgtgaag aaaaatgtat ttttcctaaa tagaaataaa 960
tgatcccatt ttttggtaaa aaaaagtatg tgagatttat tcgtaaacgt gactacttta 1020
tttctaaata agagattccc tacctgcgtc ctacaagcag ttcagaatgc catgcct 1077

```

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

cgcagggctg cttgtgatct ggtacgagga ttatgcaagt tttttgaggg acctgtgaca 60
ggaatcttct ctggttatgt taattccatg ctgcaggaat acgcaaaaaa tccatctgtc 120
aactggaaac acaaagatgc agccatctac ctagtgcacat ctttggcatc aaaagcccaa 180
acacagaagc atggaattac acaagcaaat gaacttgtaa acctaactga gttctttgtg 240
aatcacatcc tccctgattt aaaatcagct aatgtgaatg aatttcctgt ccttaaagct 300
gacggatcca aatatattat gatttttaga aatcaagtgc caaaagaaca tcttttagtc 360
tcgattcctc tcttgattaa tcattctcaa gctgaaagta ttgttgttca tacttacgca 420
gctcatgctc ttgaacggct ctttactatg cgagggccta acaatgccac tctctttaca 480
gctgcagaaa tgcgaccggt ttgtgagatt ctgctaacaa accttttcaa agctctcaca 540
cttcctggct cttcagaaaa tgaatatatt atgaaagcta tcatgagaag tttttctctc 600
ctacaagaag ccataatccc ctacatccct actctcatca ctcagcttac acagaagcta 660
ttagctgtta gtaagaaccc aagcaaacct cactttaatc actacatggt tgaagcaata 720
tgtttatcca taagaataac ttgcaaaagct aaccctgctg ctggtgtaaa ttttgaggag 780
gctttgtttt tgggtgtttac tgaaatctta caaaatgatg tgcaagaatt tattccatac 840
gtctttcaag tgatgtcttt gcttctggaa acacacaaaa atgacatccc gtcttccctat 900
atggccttat ttctcatctc ccttcagcca gtgctttggg aaagaacagg aaatattcct 960
gctctagtga ggcttcttca agcattctta gaacgcggtt caaacacaat agcaagtgtc 1020
gcagctgaca aaattcctgg gttactaggt gtctttcaga agctgattgc atccaaagcal 1080
aatgaccacc aaggttttta tcttctaaac agtataatag agcacatgcc tcttgaatcal 1140
gttgaccaat ataggaaaca aatcttcatt ctgctattcc agagacttca gaattccaaal 1200
acaaccaagt ttatcaagag ttttttagtc ttattaatt tgtattgcat aaaatatggg 1260
gcaactagcac tacaagaaat atttgatggt atacaaccaa aaatgtttgg aatggttttg 1320
gaaaaaatta ttattcctga aattcagaag gtatctggaa atgtagagaa aaagatctgt 1380
goggttggca taaccaaatt actaacagaa tgtcccccac tgatggacac tgagtatacc 1440
aaactgtgga ctccattatt acagtctttg attggtcttt ttgagttacc cgaagatgat 1500
accattcctg atgaggaaca ttttattgac atagaagata caccaggata tcagactgcc 1560
ttctcacagt tggcatttgc tgggaaaaaa gagcatgac ctgtaggtca aatggtgaat 1620
aacccccaaa ttcacctggc acagtcactt cacaagtgtg ctaccgcctg tccaggaagg 1680
gttccatcaa tggcaaaagaa ctctgtgata aatggagact ttaatgggag ggcaaaaggal 1740
tagtagtagt tctgg

```

(2) INFORMATION ON SEQ ID NO. 94:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

gttcgggcgag cgagcacctt cgacgcggtc cggggacccc tcgtcgctgt cctcccgcag 60
cggaccccggt gccccaggct cgcgctgccc ggcagggtgc tcgtgtccca ctcccggcgc 120
acgcctcccg cgagtcocgg gcccctcccg cgcctctctt ctgcgcgcgc gcgcagatcg 180
gcgccccgcg aggtccctcg gtccgggctt ctgcttgccg cggcgacggc gacttttgcc 240
gcagctcagg aagaatgtgt ctgtgaaaac tacaagctgg ccgtaaactg ctttgtgaat 300
aataatcgtc aatgccagtg tacttcagtt ggtgcacaaa atactgtcat ttgtcaaaag 360
ctggctgcca aatgtttggt gatgaaggca gaaatgaatg gctcaaaact tgggagaaga 420
gcaaaacctg aaggggccct ccagaacaat gatgggcttt atgatcctga ctgcgatgag 480
agcgggctct ttaaggccaa gcagtgaac ggcacctcca tgtgctggtg tgtgaacact 540
gctggggctc gaagaacaga caaggacact gaaataacct gctctgagcg agtgagaacc 600
tactggatca tcattgaact aaaacacaaa gcaagagaaa aaccttatga tagtaaaagt 660
ttgcggactg cacttcagaa ggagatcaca acgcgttatc aactggatcc aaaatttatc 720
acgagatttt tgtatgagaa taatgttatc actattgatc tggttcaaaa ttcttctcaa 780
aaaactcaga atgatgtgga catagctgat gtggcttatt attttgaaaa agatgttaaa 840
ggtgaatcct tgtttcattc taagaaaatg gacctgacag taaatgggga acaactggat 900
ctggatcctg gtcaaaactt aatttattat gttgatgaaa aagcacctga attctcaatg 960
cagggctctaa aagctgggtg tattgctggt attgtggttg tggatgagc agttgtgct 1020
ggaattgttg tgctggttat ttccagaaaag aagagaatgg caaagtatga gaaggctgag 1080
ataaaggaga tgggtgagat gcatagggaa ctcaatgcat aactatataa tttgaagatt 1140
atagaagaag ggaaatagca aatggacaca aattacaaat gtgtgtgcgt gggacgaaga 1200
catctttgaa ggtcatgagt ttgttagttt aacatcatat atttgtaata gtgaaacctg 1260
tactcaaaat ataagcagct tgaaactggc ttaccaatc ttgaaatttg accacaagtg 1320
tcttatatat gcagatctaa tgtaaaatcc agaacttga ctccatcggt aaaattattt 1380
atgtgtaaca ttcaaagtgt tgcattaaat atgcttcac agtaaaatct gaaaaactga 1440
tttgtgattg aaagctgcct ttctatttac ttgagtcctg tacatacata cttttttatg 1500
agctatgaaa taaaacattt taaactgaaa aaaaaaaaaa aaggc 1545

```

(2) INFORMATION ON SEQ ID NO. 95:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

g c g c g g t a t t   a t c g g g t a g a   c a t c t c g c a c   c g c g t c t c g g   a a a c c g g t a g   c g c t t g c a g c   60
a t g g c t g a c c   a a c t g a c t g a   a g a g c a g a t t   g c a g a a t t c a   a a g a a g c t t t   t t c a c t a t t t   120
g a c a a a g a t g   g t g a t g g a a c   t a t a a c a a c a   a a g g a a t t g g   g a a c t g t a a t   g a g a t c t c t t   180
g g g c a g a a t c   c c a c a g a a g c   a g a g t t a c a g   g a c a t g a t t a   a t g a a g t a g a   t g c t g a t g g t   240
a a t g g c a c a a   t t g a a c t t c c   c t g a a t t t c t   g g a c a a g g a t   g g c a a g a a a a   a t g a a a g a c a   300
c a g a c a g t g a   a g a a g a a a t g   a g a g a a g c a t   t c c g t g t g t t   t g a t a a g g a t   g g c a a g g g c t   360
a t a t g a g t g c   t g c a g a a c t t   c g c c a t g t g a   t g a c a a a c c t   t g g a g a g a a g   t t a a c a g a t g   420
a a g a a g t t g a   t g a a a t g a t c   a g g g a a g c a g   a t a t t g a t g g   t g a t g g t c a a   g t a a a c t a t g   480
a a g a g t t t g t   a c a a a t g a t g   a c a g c a a a g t   g a a g a c c t t g   t a c a g a a t g t   g t t a a a t t t c   540
t t g t a c a a a a   t t g t t t a t t t   g c c t t t t c t t   t g t t t g t a a c   t t a t c t g t a a   a a g g t t t c t c   600
c c t a c t g t c a   a a a a a a t a t g   c a t g t a t a g t   a a t t a g g a c t   t c a t t c c t c c   a t g t t t t c t t   660
c c c t t a t c t t   a c t g t c a t t g   t c c t a a a a c c   t t a t t t t a g a   a a a g t t g a t c   a a g g t a a c a t   720
g t t g c a t g t g   g c t t a c t c t g   g g g a a a t a t c   t a a g c c c t t c   t g c a c a t c t a   a a c t t a g a t g   780
g a g t t g g t c a   a a t g a g g g a a   c a t c t g g g t t   a t g c c t t t t t   t a a a g t a g t t   t t c t t t a g g a   840
a c t g t c a g c a   t g t t g t t g t t   g a a g t g t g g a   g t t g t a a c t c   t g c g t g g a c t   a t g g a c a g t c   900
a a c a a t a t g t   a c t t a a a a g t   t g c a c t a t t g   c a a a a c g g g t   g t a t t a t c c a   g g t a c t c g t a   960
c a c t a t t t t t   t t g t a c t g c t   g g t c c t g t a c   c a g a a a c a t t   t t c t t t t a t t   g t t a c t t g c t   1020
t t t t a a a c t t   g g t t t a g c c a   c t t a a a a t c t   g c t t a t g g c a   c a a t t t g c c c   c a a a a t c c a t   1080
t c c a a g t t g t   a t a t t t g t t t   t c c a a t a a a a   a a a t t a c a a t   t t a c c c a a a a   a a a   1133

```

(2) INFORMATION ON SEQ ID NO. 96:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 791 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

gccgcccgcg cggaccgccg gagaggcgcc ggccgggagcg gcggtgatgg acgggtccgg 60
ggagcagccc agaggcgggg ggcccaccag ctctgagcag atcatgaaga caggggccct120
tttgcttcag ggtttcatcc aggatcgagc agggcggaatg gggggggagg caccgagct180
ggccctggac ccggtgcctc aggatgctgc caccaagaag ctgagcgaat gtctcaagcg240
catcggggac gaactggaca gtaacatgga gctgcagagg atgattgccg ccgtggacac300
agactccccc cgagaggtct ttttcgagc ggagctgac atgtttctg acggcaactt360
caactggggc cgggttgctg cccctttcta ctttgccagc aaactgggtg tcaaggccct420
gtgcaccaag gtgccggaac tgatcagaac catcatgggc tggacattgg acttcctccg480
ggagcggctg ttgggctgga tccaagacca ggggtgggtg gacggcctcc tctcctactt540
tgggacgccc acgtggcaga ccgtgacct ctttgtggcg ggagtgtca ccgcctact600
caccatctgg aagaagatgg gctgaggccc ccagctgcct tggactgtgt ttttcctcca660
taaattatgg catttttctg ggagggtg ggattggggg acatgggcat tttcttact720
tttgraatta ttggggggtg tggggaagag tggctctgag ggggtaataa acctccttcg780
ggacacaaaa a

```

791

(2) INFORMATION ON SEQ ID NO. 97:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 599 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

tcttgccctc accatgaagt ccagcggcct ctcccccctc ctggtgctgc ttgccctggg 60
aactctggca ccttgggctg tggaaaggctc tggaaagtcc ttcaaagctg gactctgtcc120

tcttaagaaa tctgcccagt gccttagata caagaaacct gactgccaag gtgactggca180
gtgtccaggg aagaagagat gttgtcctga cacttgtggc atcaaatgcc tggatcctgt240
tgacacccca aacccaacaa ggagggaagc tgggaagtgc ccagtgaact atggccaatg300
tttgatgctt aaccccccca atttctgtga gatggatggc cagtgcgaag gtgacttgaa360
gtgttgcatg ggcattgtgt ggaaatcctg cgtttccccc gtgaaagctt gattcctgcc420
atatggagga ggctctggag tctgtctctg tgtgggtccg gtcccttcca cctgagact480
tggctccacc actgatatac tcttttgggg aaaggcttgg cacacagcag gctttcaaga540
agtgcagtt gatcaatgaa taaataaacg agcctatttc tctttgcaaa aaaaaaaaaa 599

```

(2) INFORMATION ON SEQ ID NO. 98:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 643 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

gggcccgcgg ctcgggcgta ggaggcggtg cctctgcagc aagcgtgggg cgcggggaacc 60
cgagcaggac tctccagtc tcagtcacct tggacaaaga agtgtggatc ctccagattcc120
atcttttcca actccaaggt gccatggcag agaaggtgct ggtaacaggt ggggctggct180
acattggcag ccacacgggtg ctggagctgc tggaggctgg ctacttgctt gtggtcacg240
ataacttcca taatgccttc cgtggagggg gctccctgcc tgagagcctg cggcgggtcc300
aggagctgac aggccgctct gtggagtgtg aggagatgga cattttggac caggagagccc360
tacagcgtct cttcaaaaag tacagcttta tggcggtcat ccactttgcy gggctcaagg420
ccgtgggcga gtcggtgcag aagcctctgg attattacag agttaacctg accgggacca480
tccagcttct ggagatcatg aaggccacg gggatgaaga cctggtgttc agcagctcag540
ccactgtgta cgggaacccc cagtacctgc ccccttgaat gagggccacc ccacgggggtg600
ggatgtaaca accttacgga agtccaaatt tctttatctt ttc 643

```

(2) INFORMATION ON SEQ ID NO. 99:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

ctcgagccgc tcgagccgat tcggctcgag tgccctccaga ggactggcca ctttttgcc 60
agataaagat gcacttagag atgaatatga tgatctctca gatttgaatg cagtacaaat120
ggagagtgtt cgagaatggg aaatgcagtt taaagaaaaa tatgattatg taggcagact180
cctaaaacca ggagaagaac catcagaata tacagatgaa gaagatacca aggatcacaa240
taaacaggat tgaactttgt aaacaaccaa agtcaggggc cttcagaact gcaattctta300
ctccctttca cagactgtcc ggagtctttg ggtttgattc acctgctgcg aaaaacattc360
aacaaattgt gtacaagata aattaatctc actatgaaga tttgaataac tagacattat420
ttatgctgcc aaactcattt gttgcagttg tttgtaatgt ctagtggggc ttcacatcc480
tgaaaagaag gagacaggga tttttttaa gacaaagaaa gtcacaatat tacttctttc540
cttccttttt tccctttttt ctttcttctt tctctttctt tctttttaa atatttgaa600
gacaaccaga tatgtatttg ctactcaagt gtacagatct cctcaagaaa catcaaggga660
ctcctgtgtc acatactgtg tttttatttt aacatgggtg agggaggcga cctgatcagg720
ggaggtgggg gtacacatca atttgagttg ttcaggctac tgaaacatta aaatgtgaat780
tcccaaactt ttctttttgg cattgttcgg gggataggga aatatcgtt ttaaaggagt840
cttggaatt gggtgtggga                                     860

```

(2) INFORMATION ON SEQ ID NO. 100:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

ggggggttgg ccagcctggg cgggggagag gactggctgg gcagggggcg cggcccgcc 60
cgggagaggg gggccggggg gggctgggag tatttgaggc tcggagccac cggcccgcc 120
gcggcccgag caccctcctg ccagcagcgg tccggagcca gccaacgagc ggaaaaatgg 180
agacaatttt tcgctccatg atgcgttatc tgggtctgga aaccctaaacc ctcaaggatg 240
gcctggcgca tgggggaacc agcctgctgg ggcagggggc taccagggg ctccctatcc 300
tggggcctac cccgggcagg caccctcagg ggcttatcct ggacaggcac ctccagggcg 360
ctaccctgga gcacctggag cttatcccg agcacctgca cctggagtct acccagggcg 420
accagcggc cctggggcct acccatctc tggacagcca agtggcacc gagcctacc 480
tgccactggc cctatggcg cccctgctgg gccactgatt gtgcctata acctgccttt 540
gcctggggga gtggtgcctc gcatgctgat aacaattctg ggcacggtga agcccaatgc 600
aaacagaatt gcttttagatt tccaaagagg gaatgatgtt gccttcact ttaaccacg 660
cttcaatgag aacaacagga gagtcatgtt ttgcaatata aagctggata ataactgggg 720
aagggaagaa agacagtcgg tttcccat tgaagtgagg aaaccattca aaatacaagt 780
actggttga cctgaccact tcaaggttgc agtgaatgat gctcacttgt tgcagtacaa 840
tcctcgggtt aaaaaactca atgaaatcag caaactggga atttctggtg acatagacct 900
caccagtgtc tcataatacca tgatataatc tgaaaggggc agattaaaaa aaaaaaaaga 960
atctaaacct tacatgtgta aagggttcat gttcactgtg agtgaataatt ttacattca 1020
tcaatatccc tcttgtaagt catctactta ataaatatta cagtgaataa aaaaaaaaaa 1080
aaaaaaaaaa gtcgaaaaag gagggggaag gagagagagg gaagaagaga gaggagaagg 1140
aggggggggg tgggt 1155

```

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 522 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

aaaaatattt gctggaaatt gctgtgtagg attacaggcg tgaccactgc gcccgccac 60
attcagttct tatcaaagaa ataaccaga cttaattctg aatgatacga ttatgcccaal20
tattaagtaa aaaaataaag aaaaggttat cttaaataga tcttaggcaa aataccagct180
gatgaaggca tctgatgcct tcatctgttc agtcatctcc aaaaacagta aaaataacca240
ctttttgttg ggcaatatga aatttttaaa ggagtagaat accaaatgat agaaacagac300
tgctgaatt gagaattttg atttcttaaa gtgtgtttct ttctaaattg ctgttcctta360

```

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atttgattaa ttttaattcat gtattatgat taaatctgag gcagatgagc ttacaagtat420
tgaaataaatt actaattaat cacaaatgtg aagttatgca tgatgtaaaa aatacaaaaca480
ttctaattaa aggcctttgca acacaaaaaa aaqaaaaaaa aa 522

```

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

ccagctcgcc ctgcctagcc agggggcgccc cgccccctgc ctgcccggcc accttcggga 60
gccgcttcca ataggcgcttc gccattggct ctggcgacct ccgcgcgttg ggaggtgtag 120
cgcggtcttg aacgcgctga gggccgttga gtgtcgacagg cggcgagggc gcgagtgagg 180
agcagaccca ggcacgcgcg gccgagaagg ccggggcgctcc ccacactgaa ggtccggaaa 240
ggcgacttcc gggggccttg gcacctggcg gacctccccg gagcgtcggc acctgaacgc 300
gaggcgctcc attgcgcgtg cgcgttgagg ggcttccccg acctgatcgc gagaccccaa 360
cggctggttg cgtgcctgcg gcgtctcgcc tgagctggcc atggcgagc gtgccccgtg 420
aggcgagcgc ggcgtttctc gccctgctgg gatcgctgct cctctctggg gtcctggcgg 480
ccgaccgaga acgcagcacc cagcattctt gcctgggtgc gaaggtggtg ggcagatgcc 540
gggctcccat gcctaggttg tggtaaatg tcactgacgg atcctgccag ctggttgtgt 600
atgggggctg tgacggaaac agcaataatt acctgaccaa ggaggagtgc ctcaagaaat 660
gtgccactgt cacagagaat gccacgggtg acctggccac cagcaggaat gcagcggatt 720
cctctgtccc aagtgtccc agaaggcagg attctgaaga ccactccagc gatatgttca 780
actatgaaga atactgcacc gccaacgcag tcactgggcc ttgccgtgca tccttcccac 840
gctggtactt tgacgtggag aggaactcct gcaataactt catctatgga ggctgccggg 900
gcaataagaa cagctaccgc tctgaggagg cctgcatgct ccgctgcttc cgccagcagg 960
agaatcctcc cctgccccct ggctcaaagg tggtggttct ggcggggctg ttcgtgatgg1020
tggtgatcct cttcctggga gcctccatgg tctacctgat ccgggtggca cggaggaacc1080
aggagcgtgc cctgcgcacc gtctggagct ccggagatga caaggagcag ctggtgaaga1140
acacatatgt cctgtgaccg ccctgtcgcc aagaggactg gggaagggag gggagactat1200
gtgtgagctt tttttaaata gagggattga ctcgatttg agtgatcatt agggctgagg1260
tctgtttctc tgggaggtag gacggctgct tctggtctg gcagggatgg gtttctttg1320
gaaatcctct aggaggctcc tcccgcatg gcctgcagtc tggcagcagc cccgagttgt1380
ttcctcgctg atcgatttct ttcctccagg tagagtttct tttgcttatg ttgaattcca1440
ttgctctttt tctcatcaca gaagtgatgt tggaaatcgt tcttttgttt gtctgattta1500
tggttttttt aagtataaac aaaagttttt tattagcatt ctgaaagaag gaaagtaaaa1560
tgtacaagtt taataaaaaa gggccttccc ctttagaata aaaaaaaaaa aaaaaaaaaa1620
aaaaaaaaa

```

(2) INFORMATION ON SEQ ID NO. 103:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 605 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

cctggcagct gtcggctgga aggaactggt ctgctcacac ttgctggctt gcgcatcagg 60
actggcttta tctcctgact cacgggtgcaa aggtgcactc tgcgaacggt aagtcggtcc120
ccagcgcttg gaatcctacg gccccacag cgggatcccc tcagccttcc aggtcctcaal80
ctcccgcgga cgtcgaacaa tggcctccat ggggctacag gtaatgggca tcgcgctggc240
cgtcctgggc tggctggccg tcatgctgtg ctgcgcgctg cccatgtggc gcgtgacggc300
cttcacggc agcaacattg tcacctcgca gaccatctgg gagggcctat ggatgaactg360
cgtggtgcag agcaccggcc agatgcagtg caagggtgtac gactcgctgc tggcactgcc420
gcaggacctg caggcgggcc gcgccctcgt catcatcagc atcatcgtgg ctgctctggg480
cgtgctgctg tccgtgggtg ggggcgaagt gtaacaaact tgcctggagg attaaaagcg540
ccaagggcaa gaacatgatt cgttggcggg cgtgggtgtt tctgtttggg ccggcctaata600
gggtg                                           605

```

(2) INFORMATION ON SEQ ID NO. 105:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2731 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

agggggggcgg acagacacag actatgcaga tgggagtgaa gacaaagtag tagaagtagc 60
agaggaggaa gaagtggctg aggtggagga cgatgaggat ggtgatgagg tagaggaaga 120
ggctgaggaa ccctacgaag aagccacaga gagacacaga gtctgtggaa gaggtgggtc 180
gagagggtgtg ctctgaacaa gccgagacgg ggccgtgccg agcaatgac tcccgctggg 240
actttgatgt gactgaaggg aagtgtgccc cattctttta cggcggtatg ggcggcaacc 300
ggaacaactt tgacacagaa gagtactgca tggccgtgtg tggcagcgcc attcctacaa 360
cagcagccag taccctgat gccgttgaca agtatctcga gacacctggg gatgagaatg 420
aacatgcccc tttccagaaa gccaaagaga ggcttgaggc caagcaccga gagagaatgt 480
cccaggtcac gagagaatgg gaagaggcag aacgtcaagc aaagaacttg cctaaagctg 540
ataagaaggc agttatccag catttccagg agaaagtggg atctttggaa caggaagcag 600
ccaacgagag acagcagctg gtggagacac acatggccag agtggaagcc atgctcaatg 660
accgcgcgcg cctggccctg gagaactaca tcaccgctct gcaggctgtt cctcctcggc 720
ctcgtcacgt gttcaatatg ctaaagaagt atgtccgcgc agaacagaaq gacagacagc 780
acaccctaaa gcatttcgag catgtgcgca tgggtgatcc caagaaagcc gctcagatcc 840
ggtcccaggc tatgacacac ctccgtgtga tttatgagcg catgaatcag tctctctccc 900
tgctctacaa cgtgcctgca gtggcgcagg agattcagga tgaagttagt gagctgcttc 960
agaaagagca aaactattca gatgacgtct tggccaacat gattagttaa ccaaggatca 1020
gttacggaaa cgatgctctc atgccatctt tgaccgaaac gaaaaccacc gtggagctcc 1080
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aattggtgtt ctttgcagaa gatgtgggtt caaacaagg tgcaatcatt ggactcatgg 1380
tgggcggtgt tgtcatagcg acagtgatcg tcatcacctt ggtgatgctg aagaagaaac 1440
agtacacatc cattcatcat ggtgtggtag aggttgacgc cgctgtcacc ccagaggagc 1500
gccacctgtc caagatgcag cagaacggct acgaaaatcc aacctacaag tcttttagag 1560
agatgcagaa ctagaccccc gccacagcag cctctgaagt tggacagcaa aaccattgct 1620
tcactaccca tcggtgtcca tttatagaat aatgtgggaa gaaacaaacc cgttttatga 1680
tttactcatt atcgctttt gacagctgtg ctgtaacaca agtagatgcc tgaacttgaal 1740
ttaatccaca catcagtaat gtattctatc tctctttaca ttttgggtct tatactacat 1800
tattaatggg ttttgtgtac tgtaaagaat ttagctgtat caaactagt catgaataga 1860
ttctctctcg attatttatt acatagcccc ttagccagtt gtatattatt cttgtgggtt 1920
gtgacccaat taagtcctac tttacatatg ctttaagaat cgatggggga tgcttcatgt 1980
gaacgtggga gttcagctgc ttctcttgcc taagtattcc tttcctgate actatgcatt 2040
ttaaagttaa acatttttaa gtatttcaga tgcttttag agatttttt tccatgactg 2100
cattttactg tacagattgc tgcttctgct atatttgta tataggaatt aagaggatac 2160
acacgtttgt ttcttcgtgc ctgttttatg tgcacacatt aggcattgag acttcaagct 2220
tttctttttt tgtccacgta tctttgggtc tttgataaag aaaagaatcc ctgttcattg 2280
taagcacttt tacggggcgg gtggggagg gtgctctgct ggtcttcaat taccaagaat 2340
tctccaaaac aattttctgc aggatgattg tacagaatca ttgcttatga catgatcgct 2400
ttctacactg tattacataa ataaattaaa taaataacc ccgggcaaga cttttctttg 2460
aaggtagact acagacatta aataatcgaa gtaattttgg gtggggagaa gaggcagatt 2520
caattttctt taaccagttc gaagtttcat ttatgataca aaagaagatg aaaatggaag 2580
tggcaatata aggggatgag gaaggcatgc ctggacaaac ccttctttta agatgtgtct 2640
tcaatttgta taaaatgggt ttttcatgta aataaataca ttcttgagg agccaaaaaa 2700
aactatatta ctggcaggtt tataatatgg c 2731

```

(2) INFORMATION ON SEQ ID NO. 106:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2194 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

gaattcagaa gttaatgatg ttgggtaaga gaacaatggt aagagagcaa tctaagaata 60
tatcacctac tttaatTTTA tatgagagta catggaggta gctgtgatgt ggaaatgtag 120
cactgctcct acccacgcag atttattcca gtgaaacaac aactggaact tcaagtaact 180
cctcccagag tacttccaac tctgggttgg ccccaaatcc aactaatgcc accaccaagg 240
cggctgggtg tgccctgcag tcaacagcca gtctcttcgt ggtctcactc tctcttctgc 300
atctctactc ttaagagact caggccaaga aacgtcttct aaatttcccc atcttctaaa 360
cccaatccaa atggcgtctg gaagtccaat gtggcaagga aaaacagggtc ttcacggaat 420
ctactaattc cacacctttt attgacacag aaaatgttga gaatcccaaa tttgattgat 480
ttgaagaaca tgtgagagggt ttgactagat gatggatgcc aatattaaat ctgctggagt 540
ttcatgtaca agatgaagga gaggcaacat ccaaaaatagt taagacatga tttccttgaa 600
tgtggcctga gaaatatgga cacttaatac taccttgaaa ataagaatag aaataaagga 660
tggtgatttg gaatggagat tcagttttca tttgggtcat taattctata aggccataaa 720
acaggtaata taaaaagctt ccatgattct atttatatgt acatgagaag gaactccag 780
gtgttactgt aattcctcaa cgtattgttt cgacagcact aatttaatgc cgataactc 840
tagatgaagt ttacattgt tgagctattg ctgttctctt gggaactgaa ctacttttcc 900
tcttgaggct ttggatttga cattgcattt gaccttttat gtagtaattg acatgtgcca 960
gggcaatgat gaatgagaat ctaccccccag atccaagcat cctgagcaac tcttgattat 1020
ccatattgag tcaaatggta ggcatttctc atcacctgtt tccattcaac aagagcacta 1080
cattcattta gctaaacgga ttccaaagag tagaattgca ttgaccgcga ctaatttcaa 1140
aatgcttttt attattatta ttttttagac agtctcactt tgtcgcccag gccggagtgc 1200
agtgggtgca tctcagatca gtgtaccatt tgccctcccg gctcaagcga ttctcctgcc 1260
tcagcctccc aagtagctgg gattacaggc acctgccacc atgcccggct aatttttgta 1320
atttttagtag agacaggggt tcaccatgtt gccagggctg gtttcgaact cctgacctca 1380
ggatgatccac ccgcctcggc ctcccaaagt gctgggatta caggcttgag ccccgcgccc 1440
cagccatcaa aatgcttttt atttctgcat atgttgaata ctttttacia tttaaaaaaa 1500
tgatctgttt tgaaggcaaa attgcaaatt ttgaaattaa gaaggcaaaa atgtaaaagg 1560
gtcaaaacta taaatcaagt atttggaag ttgaagactgg aagctaattt gcattaaatt 1620
cacaaaactt tatactcttt ctgtatatac attttttttc tttaaaaaac aactatggat 1680
cagaatagcc acatttagaa cactttttgt tatcagtcaa tattttttaga tagttagaac 1740
ctggctctaa gcctaaaagt gggcttgatt ctgcagtaaa tcttttacia ctgcctcgac 1800
acacataaac ctttttaaaa atagacactc cccgaagtct tttgttcgca tggtcacaca 1860
ctgatgctta gatgttccag taatctaata ttggccacagt agtcttgatg accaaagtcc 1920
tttttttcca tcttttagaaa actacatggg aacaaaacaga tcgaacagtt ttgaagctac 1980
tgtgtgtgtg aatgaacact cttgctttat tccagaatgc tgtacatcta ttttgatttg 2040
tatatttgtt ttgtgtattt acgctttgat tcatagtaac ttcttatgga attgatttgc 2100
attgaacaca aactgtaaat aaaaagaaat ggctgaaaga gcaaaaaaaa aggaaagaaa 2160
aaagaaaaaa aaaagaaaaa aaaaaggggg aggc

```

2194

(2) INFORMATION ON SEQ ID NO. 107:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

cggaagggtg accttggatg aattttgacg agaacaagtt cgtggaccga agaagatggg 60
ggccgcacgc ccaggcccg gccccgacga ggccgaggtg gacacctgcc ccctgcgcaa 120
aggaacatg aaacagaccc tacaggcagc tctgaagaac cccctatca acaccaagag 180
tcaggcagtg aaggaccggg caggcagcat tgtcttgaag gtgctcatct cttttaaaagc 240
taatgatata gaaaaggcag ttcaatctct ggacaagaat ggtgtggatc tcctaataa 300
gtatatattt aaaggatttg agagcccgtc tgacaatagc agtgcctatg tactgcaatg 360
gcatgaaaag gcacttgctg ctggaggagt aggggtccatt gttcgtgtct tgactgcaag 420
aaaaactgtg tagtctggca ggaagtggat tatctgcctc gggagtggga attgctggta 480
caaagacca aacaaccaa tgccaccgct gccctgtggg tagcatctgt ttctctcagc 540
tttgccttct tgctttttca tatctgtaaa gaaaaaaatt acatatcagt tgccttttaa 600
tgaaaatttg gataatatag aagaaattgt gttaaaaatg aagtgtttca tcctttcaaa 660
accatttcag tgatgtttat accaatctgt atatagtata atttacattc aagtttaatt 720
gtgcaacttt taacccctgt tggctgggtt tttgttctgt tttgttttgt attattttta 780
actaatactg agagatttgg tcagaatttg aggccagttt cctagctcat tgctagtcag 840
gaaatgatat ttataaaaaa tatgagagac tggcagctat taacattgca aaactggacc 900
atatttcctt tatttaataa gcaaaatatg tttttggaat aagtgggtggg tgaataccac 960
tgccaagtta tagctttgtt tttgcttgcc tcctgattat ctgtactgtg ggtttaagta 1020
tgctactttc tctcagcatc caataatcat ggccctcaa tttatttgtg gtcacccagg 1080
gttcagagca agaagtcttg ctttatacaa atgtatccat aaaatatcag agcttgttgg 1140
gcatgaacat caaacttttg ttccactaat atggctctgt ttggaaaaaa ctgcaaatca 1200
gaaagaatga ttgacagaaa gaaagaaaaa ctatggtgta atttaaactc tgggcagcct 1260
ctgaatgaaa tgctactttc tttagaaata taatagctgc cttagacatt atgaggtata 1320
caactagtat ttaagatacc atttaatatg ccccgtaaat gtcttcagtg ttcttcaggg 1380
tagttgggat ctcaaaagat ttggttcaga tccaaacaaa tacacattct gtgttttagc 1440
tcagtgtttt ctaaaaaaag aaactgccac acagcaaaaa attgtttact ttgttggaca 1500
aaccaaatca gttctcaaaa aatgaccggt gcttataaaa agttataaat atcgagttag 1560
tctaaaacaa accacctgac caagagggaa gtgagcttgt gcttagtatt tacattggat 1620
gccagttttg taatcactga cttatgtgca aactggtgca gaaattctat aaactctttg 1680
ctgtttttga tacctgcttt ttgtttcatt ttgttttgtt ttgtaaaaat gataaaactt 1740
cagaaaataa aatgtcagtg ttgaataaaa taaaaaaaca aattgaagaa gaggatggag 1800
atttcgactt gg

```

1812

(2) INFORMATION ON SEQ ID NO. 108:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 890 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

aacgactcct ggtaccttgc tcccattact tcccgttttc tcgatctgct gctcgtctca 60
ggctcgtagt tcgccttcaa catgccggaa ccagcgaagt ccgctccccg gcccaagaag120
ggctcgaaga aagccgtgac taaggcgcag aagaaggacg gcaagaagcg caaggcagcc180
gcaaggagag ctactccgta tacgtgtaca aggtgctgaa gcagggtccac cccgacaccg240
gcatctcttc taaggccatg ggaatcatga actccttcgt caacgacatc ttcgaacgca300
tcgcggggtga ggcttccccg ctggcgcatc acaacaagcg ctcgaccatc acctccaggg360
agatccagac ggccgtgctg ctgctgctgc ccggggagtt ggccaagcac gccgtgtccg420
agggcaccaa ggccgtcacc aagtacacca gcgctaagta aacttgccaa ggagggactt480
tctctggaat ttcctgatat gaccaagaaa gcttcttctc aaaagaagca caattgcctt540
cggttacctc attatctact gcagaaaaga agacgagaat gcaaccatac ctgatggac600
ttttccacaa gctaaagctg gcctcttgat ctcatcaga ttccaaagag aatcattttac660
aagttaattt ctgtctcctt ggtccattcc ttctctctaa taatcattta ctgttcttca720
aagaattgtc tacattaccc atctcctctt ttgcctctga gaaagagtat ataagcttct780
gtacccactt ggggggttgg ggtaatatc tgtggtcctc agccctgtac cttaataaat840
ttgtatgcct tttctcttaa aaaaaaaaaa aagaagaagg aagaggatgc 890

```

(2) INFORMATION ON SEQ ID NO. 110:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2627 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

ggcacgagat gtgaaaaggt tttgtgtaca ccacctccaa aaataaaaaa tggaaaacac 60
accttttagt aagtagaagt atttgagtat cttgatgcag taacttatag ttgtgatcct 120
gcacctggac cagatccatt ttcacttatt ggagagagca cgattttatt tggtgacaat 180
tcagtgtgga gtcgtgctgc tccagagtgt aaagtgggca aatgtcgatt tccagtagtc 240
gaaaatggaa aacagatata aggatttgga aaaaaatttt actacaaagc aacagttatg 300
tttgaatgag ataagggttt ttacctcgat ggcagcgaca caattgtctg tgacagtaac 360
agtacttggg atccccaggt tccaaagtgt cttaaagtgt cgacttcttc cactacaaaa 420
tctccagcgt ccagtgcctc aggtcctagg cctacttaca agcctccagt ctcaaattat 480
ccaggatata ctaaacctga ggaaggaata cttgacagtt tggatgtttg ggtcattgct 540
gtgattgtta ttgccatagt tgttggagtt gcagtaattt gtgttgtccc gtacagatat 600
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actaaatcaa ccactccagc agagcagaga ggctgaatag attccacaac ctgggtttgcc 720
agttcatctt ttgactctat taaaatcttc aatagtgttt attctgtagt ttcactctca 780
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gatgtctctt tgaacttgt atgaatttgg gtatgaacag attgcctgct tccccttaaa 900
taacacttag atttatttga ccagtcagca cagcatgcct ggttgtatta aagcagggat 960
atgctgtatt ttataaaatt ggcaaaatta gagaaatata gttcacaatg aaattatatt 1020
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atgtgtggca tttgttttca ctttttaaaa catccctaac tgatcgaata tatcagtaat 1380
ttcagaatca gatgcacctt ttcataagaa gtgagaggac tctgacagcc ataacaggag 1440
tgccacttca tgggtcggaag tgaacactgt agtcttgttg ttttcccaaa gagaactccg 1500
tatgttctct taggttgagt aacccactct gaattctggt tacatgtgtt tttctctccc 1560
tccttaataa aagagagggg ttaaaccatgc cctctaaaag taggtggttt tgaagagaat 1620
aaattcatca gataacctca agtcacatga gaattcttagt ccatttacat tgccttggct 1680
agtaaaagcc atctatgtat atgtcttacc tcactccta aaaggcagag tacaagtaaa 1740
gccatgtatc tcaggaaggt aacttcattt tgtctatttg ctgttgattg tacciaaggag 1800
tggagaagat aaatatagct caggtagcac tttatactca ggcagatctc agccctctac 1860
tgagtccctt agccaagcag tttctttcaa agaagccagc aggcgaaaag cagggactgc 1920
cactgcattt catatcacac tgttaaaagt tgtgttttga aattttatgt ttagtgcac 1980
aaattgggccc aaagaaacat tgccttgagg aagatatgat tggaaaatca agagtgtaga 2040
agaataaata ctgttttact gtccaaagac atgtttatag tgcctgttaa atgttcctt 2100
cctttgtagt ccttggaag atgctttagg aagataaaaag tttgaggaga acaaacagga 2160
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gcaattacta agaagcagat aatggtgttt tttagaaacc taattgaagt atattcaacc 2280
aaatacttta atgtataaaa taaatattat acaatatact tgtatagcag tttctgcttc 2340
acatttgatt ttttcaaatt taatatttat attagagatc tatatatgta taaatatgta 2400
ttttgtcaaa tttgttactt aaatatatag agaccagttt tctctggaag tttgtttaaa 2460
tgacagaagc gtatatgaat tcaagaaaaa ttaagctgca aaaaatgtatt tgctataaaa 2520
tgagaagtct cactgataga ggttctttat tgctcatttt ttaaaaaatg gactcttgaa 2580
atctgttaaa ataaaattgt acatttgga aaaaaaaaaa gccaaaaa 2627

```

(2) INFORMATION ON SEQ ID NO. 111:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 976 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

ctcgagccgc gagattcccc cgaagttctc catgaagcgc ctcaccgccc gccatcatgc 60
cgtcatcgtg gtggtcgtgg tggccctcgt cgccggcatg gccgtcctgg tgatcaccaal20
ccggagaaag tcggggaagt acaagaaggt ggagatcaag gaactggggg agttgagaaal80
ggaaccgagc ttgtaggtac ccggcggggc aggggatggg gtggggtacc ggatttcggt240
atcgtccocag acccaaagtga gtcacgcttc ctgattcctc ggcgcaaagg agacgtttat300
cctttcaaat tcttgccttc cccctccctt ttgcgcacac accaggttta atagatcctg360
gccacagggg ctcctttctt tctcacttct gtcttgaagg aagcatttct aaaatgtatc420
ccctttcggg ccaacaacag gaaacctgac tggggcagtg aaggaaggga tggcatagcg480
ttatgtgtaa aaaacaagta tctgtatgac aaccgggat cgtttgcaag taactgaatc540
cattgcgaca ttgtgaaggc ttaaagtgtt ttagatggga aatagcggtt ttatcgccctt600
gggtttaaat tatttgatga gttccacttg tatcatggcc taccgagga gaagaggagt660
ttgttaactg ggcctatgta gtagcctcat ttaccatcgt ttgtattact gaccacatat720
gcttgtcact gggaaagaag cctgtttcag ctgcctgaac gcagtttgga tgtctttgag780
gacagacatt gcccggaaac tcagtcatt tattcttcag cttgccetta ctgccactga840
tattggtaat gttctttttt gtaaaatgtt tgtacatatg ttgtctttga taatgttgct900
gtaatttttt aaaataaaac acgaatttaa taaaatatgg gaaaggcaca caaaaaaaaa960
aaaaaaaaaa aaaaac

```

976

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1427 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

ctccgggggt gactgcctct tccagggcgg gcggtgtggt gcacgcattg ctgtgctcca 60
actccctcag ggctgtgttt gccgcactct gctgctatga gcttcctcaa aagtttcccg 120
ccgcctgggc cagcggaggg gctcctgcgg cagcagccag acactgaggc tgtgctgaac 180
gggaaggggc tcggcactgg taccctttac atcgctgaga gccgcctgtc ttggttagat 240
ggctctggat taggattctc actggaatac cccaccatta gtttacatgc attatccagg 300
gaccgaagtg actgtctagg agagcatttg tatgttatgg tgaatgccaa atttgaagaa 360
gaatcaaaaag aacctgttgc tgatgaagaa gaggaagaca gtgatgatga tgttgaacct 420
attactgaat ttagatttgt gcctagtgtat aaatcagcgt tggaggcaat gttcactgca 480
atgtgcgaat gccaggcctt gcctccagat cctgaggatg aggattcaga tgactacgat 540
ggagaagaat atgatgtgga agcacatgaa caaggacagg gggacatccc tacattttac 600
acctatgaag aaggattatc ccctctaaca gcagaaggcc aagccacact ggagagatta 660
gaaggaatgc tttctcagtc tgtgagcagc cagtataata tggctggggg caggacagaa 720
gattcaataa gagattatga agatgggatg gaggtggata ccacaccaac agttgctgga 780
cagtttgagg atgcagatgt tgatcactga aaatgattta tgcaagttta agattctgct 840
cctaagtgtg ggagagaact tgggtgcctct tccactctgg agtgaagtta atgaaagtct 900
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taaccaagag ggtatttgta gtttactatt taccctaaaa ctttctgtgt ctgggtaccc 1080
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atgtggtgaa aatgcacagg agcttggtag actgcggggg aaagagagag ctcccttcgc 1200
catgttttac cagtctgctg ttataacctc tctgggatga tcctttaatt tccagccttt 1260
taggttagtt tctgtaacag aacaagttag tctgggatga agtcctcaaa gtacttcaaa 1320
tggttaattgt tttgtttttg taatagctta acaataaac ctaggttttc tatattaaaa 1380
aaaaaaaaa aaaaaaaaaa aaggtacctg ccctaataat attctgc 1427

```

(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2639 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

tccctatctt acccttcccg attctccttt tttcttttct ttttttatat ggctttcttc 60
ttttctttct ttcttttttc ttcccttttt tatttgacca gtgtaaataa caaacattta 120
ttggtgtcac ttatggtaga aaaaacttcc tacaccagat gcacatgacc cagttgttaa 180
atagaacatt ttgaagggtga acacacaccc taaccacaggt tttttaccog ctttttaaga 240
tggccaattc ttcttctccc ccccacccaa agacatgtga gcaactgcta atgaaaagca 300
gtaaacagcc gcttaggcta tagcagtttc aactccactc tgagggtgaag attccaatta 360
cattcgagac ttaagtctct tcaatttttt cctaacaaaa gtctctgagt ccagtattta 420
caatattaca gcactagcag atcagtgctc acaactcctc tttttctgct gtatcctctt 480
caccagttgg gggaggggcct gcacttccat agagtttgct gataattggg tgaacaattt 540
cttccagttc cttcttctta gctttgaagt cttcaatgtc agcatcttgg tggctttcca 600
gccattcaat cttttctttt acagcttttt ccattggtct cttatcttca gaggaaagtt 660
tacctcccag cttttcttta tctccaatct gattctttag agaataggca tagctttcca 720
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catcattaac catcctttctg atttcttcag gtgtcaggcg attctgggtc ttggtgattg 840
tgatcttatt ttgttccctt gtacccttgt cttcagctgt cactcgaaga ataccattca 900
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ccttcttttc caaataagcc tcagcgggtt ctttcatatt agtgagaacc atggtatggg 2040
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tagttttctt ttcaaccacc ttgaacggca agaacttgat gtctgtctgc acagacgggt 2160
cattccacgt gcggccgatg agccgcttgg cgtcaaagac cgtgttctgc ggttggagg 2220
tgagctgggt cttggcggca tcgccaatca gacgttcccc ttcaggagtg aaggcgacat 2280
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ccacgaacca ggcgaagggc aggtctagaa atacaggccg cggcgcttcc ctctcacact 2639
cgcgaaacac cccaataggt caatctgtct gtgctgtctt ggccggcacc gacccttag

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(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 634 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

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ctccccgcgcg cgcggttaaa tccccgcacc tgagcatcgg ctcacacctg caccgccgcc 60
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ctgctgctgt tcggcttcac cctagtctca ggcacaggag cagagaagac tggcgtgtgc180
cccgagctcc aggtgacca gaactgcacg caagagtgcg tctcggacag cgaatgcgcc240
gacaacctca agtgctgcag cgcgggctgt gccaccttct gctctctgcc caatgataag300
gagggttctt gccccaggt gaacattaac ttccccagc tcggcctctg tcgggaccag360
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gtgtcctgtg tcaactccaa ttcttgagct ccagccacca ccaggctgag cagtgaggag480
agaaagtttc tgcttgccc tgcattctgt tccagcccac ctgccctccc ctttttcggg540
actctgtatt ccctcttggt ctgaccacag cttctccctt tcccaaccaa taaagtaacc600
actttcagca aaaaaaaaaa aaaaaaaaca aaaa 634
```

(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 719 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

gtcgaactttt tttttttttt ttttaacatgg aaaagtattt ttaaaaaatcg aataaatccta 60
ttcaagtcata ccagtggttaa ccccggtgtg ctccctgcca gtctgttcct ccccatggga120
gtcacacaaaa atgaaaaatct cctagaaaaga gaagacaaaag acccgcaaaa gatgtatgcc180
accatctatg agctgaaaaga agacaagagc tacaatgtca cctccgtcct gtttaggaaa240
aagaagtgtg actactggat caggactttt gtccaggtt gccagcccgg cgagttcacg300
ctgggcaaca ttaagagtta ccttggttta acgagttacc tcgtccgagt ggtgagcacc360
aactacaacc agcatgctat ggtgttcttc aagaaagtgt ctcaaaacag ggagtacttc420
aagatcaccc tctacgggag aaccaaggag ctgacttcgg aactaaagga gaacttcac480
cgcttctcca aatctctggg cctccctgaa aaccacatcg tcttccctgt cccaatcgac540
cagtgtatcg acggctgagt gcacaggtgc cgccagctgc cgcaccagcc cgaacaccat600
tgaggagact gggagacctt cccacagtg ccacccatgc agctgtccc caggccaccc660
cgctgatgga gccccacctt gtctgctaaa taaacatgtg ccctcaaaaa aaaaaaaaaa 719

```

(2) INFORMATION ON SEQ ID NO. 116:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 494 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

gtcgataacg ccagacgcaa gacgccgggc ctacagcggg agcgtgagga aagccgtgcg 60
ttgcgttcca aggcattctg gagcccgcg agtatacacc atgagcaaag ctccacctcc120
cgagttgaaa aaatttatgg acaagaagtt atcattgaaa ttaaattggtg gcagacatgt180
ccaaggaata ttgcggggat ttgatccctt tatgaacctt gtgatatagtg aatgtgtgga240
gatggcgact agtggacaac agaacaatat tggaaatggtg gtaatacgag gaaatagtat300
catcatgtta gaagccttgg aacgagtata aataatggct gttcagcaga gaaacccatg360
tctctctctc atagggcctg ttttactatg atgtaaaaat taggtcatgt acattttcat420
attagacttt ttgttaaata aacttttgta atagtcaaaa aaaagtttgg tctcatctac480
cttataatat ctgc

```

494

(2) INFORMATION ON SEQ ID NO. 117:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

acggggctga ctacgctcaa agctccattg ttagatcctt tctgtcctcc ttcctggctc 60
ctccttccctc ccacccctc taataggctc ataagtgggc tcaggcctct ctgcggggct 120
cactctgcgc ttcacccatgg ctttcattgc caagtccctc tatgacctca gtgccatcag 180
cctggatggg gagaaggtag atttcaatac gttccggggc agggccgtgc tgattgagaa 240
tgtggcttcg ctctgaggca caaccacccg ggacttcacc cagctcaacg agctgcaatg 300
ccgctttccc aggcgccttg tggtccttgg cttcccttgc aaccaatttg gacatcagga 360
gaactgtcag aatgaggaga tcctgaacag tctcaagtat gtccgtcctg ggggtggata 420
ccagcccacc ttcacccctg tccaaaaatg tgagggtgaat gggcagaacg agcatcctgt 480
cttcgcctac ctgaaggaca agctccctta cccttatgat gacctttt ccctcatgac 540
cgatcccaaag ctcatcattt ggagccctgt gcgccgctca gatgtggcct ggaactttga 600
gaagtccctc atagggccgg agggagagcc cttccgacgc tacagccgca ccttcccaac 660
catcaacatt gagcctgaca tcaagcgcc ctttaaagtt gccatataga tgtgaactgc 720
tcaacacaca gatctctac tccatccagt cctgaggagc cttaggatgc agcatgcctt 780
caggagacac tgctggacct cagcattccc ttgatatcag tccccttcac tgcagagcct 840
tgcccttccc ctctgcctgt ttccttttcc tctcccaacc ctctggttgg tgattcaact 900
tgggctccaa gacttgggta agctctgggc cttcacagaa tgatggcacc ttcctaaacc 960
ctcatgggtg gtgtctgaga ggcgtgaagg gcttgagacc actctgctag aagagaccaal1020
taaaaggcag gtgtggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa

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1065

(2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 648 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

ggactgccgt cgtagtctc cggcgagttg ttgcctgggc tggacgtggt tttgtctgct 60
ggcccccgtc ttgcgctct cgtttcattt tctgcagcgc gccagcagga tggcccacaal20
gcagatctac tactcggaca agtacttcga cgaacactac gagtaccggc atgttatgtt180
acccagagaa ctttccaaac aagtacctaa aactcatctg atgtctgaag aggagtggag240
gagacttggt gtccaaacaga gtctaggctg ggttcattac atgattcatg agccagaacc300
acatatctct ctcttttagac gacctcttcc aaaagatcaa caaaaatgaa gtttatctgg360
ggatcgtaa atctttttca aatttaattgt atatgtgtat ataaggtagt attcagtga420
tacttgagaa atgtacaaat ctttcaccca tacctgtgca tgagctgtat tcttcacagc480
aacagagctc agttaaatgc aactgcaagt aggttactgt aagatgttta agataaaagt540
cttccagtc agtttttctc ttaagtgcct gtttgagttt actgaaacag tttacttttg600
ttcaataaag tttgtatgtt gcatttcaaaa aaaaaaaaaa aaagtcga 648

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(2) INFORMATION ON SEQ ID NO. 121:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1842 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ctcgagccgc tcgagccgct gctctctgga gggggtagag atcaaaggcg gtccttccg 60
acttctccaa gagggccagg cactggagta cgtgtgtcct tctggcttct acccgtaacc 120
tgtgcagaca cgtacctgca gatctacggg gtcctggagc accctgaaga ctcaagacca 180
aaagactgtc aggaaggcag agtgcagagc aatccactgt ccaagaccac acgacttcga 240
gaacggggaa tactggcccc ggtctcccta ctacaatgtg agtcatgaga tctctttcca 300
ctgctatgac ggttacactc tccggggctc tgccaatcgc acctgccaag tgaatggccg 360
gtggagtggg cagacagcga tctgtgacaa cggagcgggg tactgctcca acccgggcat 420
ccccattggc acaagggaag tgggcagcca gtaccgcctt gaagacagcg tcacctacca 480
ctgcagccgg gggcttacct tgcgtggctc ccagcggcga acgtgtcagg aagggtggctc 540
ttggagcggg acggagcctt cctgccaaga ctccctcatg tacgacaccc ctcaagaggt 600

ggccgaagct ttctgtctt ccctgacaga gaccatagaa ggagtcgatg ctgagggatgg 660
gcacggccca ggggaacaa agaagcggaa gatcgtcctg gacccttcag gctccatgaa 720
catctacctg gtgctagatg gatcagacag cattggggcc agcaacttca caggagccaa 780
aaagtgtcta gtcaacttaa ttgagaaggt ggcaagttat ggtgtgaagc caagatatgg 840
tctagtgaac tatgccacat accccaaaat ttgggtcaaa gtgtctgaag cagacagcag 900
taatgcagac tgggtcacga agcagctcaa tgaaatcaat tatgaagacc acaagttgaa 960
gtcagggact aacaccaaga aggccctcca ggcagtgtac agcatgatga gctggccaga 1020
tgacgtccct cctgaaggct ggaaccgcac ccgccatgtc atcatcctca tgactgatgg 1080
attgcacaac atgggcgggg acccaattac tgtcattgat gagatccggg acctgctata 1140
cattggcaag gatcgcaaaa acccaaggga ggattatctg gatgtctatg tgtttgggg 1200
cgggcctttg gtgaaccaag tgaacatcaa tgctttggct tccaagaaag acaatgagca 1260
acatgtgttc aaagtcaagg atatggaaaa cctggaagat gttttctacc aaatgatcga 1320
tgaaaagccag tctctgagtc tctgtggcat ggtttgggaa cacaggaagg gtaccgatta 1380
ccacaagcaa ccatggcagg ccaagatctc agtcattcgc ccttcaaagg gacacgagag 1440
ctgtatgggg gctgtgggtgt ctgagtactt tgtgttgaca gcagcacatt gtttcaactg 1500
ggatgacaag gaacactcaa tcaaggtcag cgtaggaggg gagaagcggg acctggagat 1560
agaagtatgc ctatttcacc ccaactacaa cattaatggg aaaaaagaag caggaattcc 1620
tgaattttat gactatgacg ttgccctgat caagctcaag aataagctga aatatggcca 1680
gactatcagg cccatttgtc tcccctgcac cgaggggaaca actcgagctt tgaggcttcc 1740
tccaactacc acttgccagc aacaaaagga agagctgctc cccgcagaag agcaaagaaa 1800
gctgtgtttg tccgggggga gaaaaaacc gccccggggg gg

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1842

(2) INFORMATION ON SEQ ID NO. 122:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

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ggcgggtata aaagccccac ccaggccagc cggtcttgct cagcatttgg ggacgctctc 60
agctctcggc gcacggccca gcttccttca aaatgtctac tggtcacgaa atcctgtgca 120
agctcagctt ggagggtgat cactctacac cccaagtgc atatgggtct gtcaaagcct 180
atactaactt tgatgctgag cgggatgctt tgaacattga aacagccatc aagaccaaag 240
gtgtggatga ggtcaccatt gtcaacattt tgaccaaccg cagcaatgca cagagacagg 300
atattgcctt cgcctaccag agaaggacca aaaaggaact tgcacagca ctgaagtcag 360
ccttatctgg ccacctggag acggtgattt tgggcctatt gaagacacct gctcagtatg 420
acgcttctga gctaaaagct tccatgaagg ggctgggaac cgacgaggac tctctcattg 480
agatcatctg ctccagaacc aaccaggagc tgcaggaaat taacagagtc tacaaggaaa 540

tgtacaagac tgatctggag aaggacatta tttcggacac atctgggtgac ttccgcaagc 600
tgatgggtgc cctggcaaaag ggtagaagag cagaggatgg ctctgtcatt gattatgaac 660
tgattgacca agatgctcgg gatctctatg acgctggagt gaagaggaaa ggaactgatg 720
ttcccaagtg gatcagcatc atgaccgagc ggaggggccc cacctccaga aagtatttga 780
taggtacaag agttacagcc cttatgacat gttggaaaagc atcaggaaaag aggttaaagg 840
agacctgcaa aatgctttcc tgaacctggg tcagtgcatt cagaacaagc cctctgattt 900
tgctgatcgg ctgtatgact ccatagaagg caaggggacg cgagataagg tctctgatcag 960
aatcatggtc tcccgccagt aagtggacat gttgaaaatt aggtctgaat tcaagagaaa1020
gtacggcaag tccctgtact attatatcca gcaagacact aaggggcgact accagaaagc1080
gctgctgtac ctgtgtgggt gagatgactg aagcccgaca cggcctgagc gtccagaaa1140
gggtgctcacc atgcttccag ctaacagggtc tagaaaacca gcttgcgaaat aacagtcccc1200
gtggccatcc ctgtgagggt gacgttagca ttacccccc aa cctcatttta gttgcctaag1260
cattgcctgg ccttctctgc tagtctctcc tghtaagccaa agaaatgaac attccaagga1320
gttggaagtg aagtctatga tgtgaaacac tttgcctcct gtgtactgtg tcataaacag1380
atgaataaac tgaatttcta ctttagaaac acgtactttg tggccctgct ttcaactgaa1440
ttgtttgaaa attaaacgtg cttgggggttc agctggtgag gctgtccctg taggaagaaa1500
gctctgggac tgagctgtac agtatggttg cccctatcca agtgtcgcta ttaagttaal560
atataaatga aataaaataa aataaaatca aaaaaa 1596

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(2) INFORMATION ON SEQ ID NO. 123:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

gtcgcagctg accctcgctc ccgccccccg ctggagtcgg acgtggaagt tgctggctga 60
ctgggcttgc gaggaaccg cctcgagct gcagccgaag gcaaggaatc actgaagatc 120
ggcgagggag gacagggggg tcatcatggg tggcttttcc tcaagtatat tttccagtct 180
gtttggaact cgggaaatga gaattttaat tttgggatta gatggagcag gaaaaaccac 240
aattttgtac agattacaag tgggagaagt tgttactact atacctacca ttggatttaa 300
tgtagagacg gtgacgtaca aaaaccttaa attccaagtc tgggatttag gaggacagac 360
aagtatcagg ccatactgga gatgttacta ttcaaacaca gatgcagtca tttatgtagt 420
agacagtgtg gaccgagacc gaattggcat ttccaaatca gagttagttg ccattgttga 480
ggaagaagag ctgagaaaaa ccatttttagt ggtgtttgca aataaacagg acatggaaca 540
ggccatgact tcctcagaga tggcaaattc acttgggtta cctgccttga aggaccgaaa 600
atggcagata ttcaaaacgt cagcaaccaa aggcaccggc cttgatgagg caatggaatg 660
gttagttgaa acattaaaaa gcagacagta attcagttcc ttcttctccc ctgaaatgaa 720
gactacatca cctctctccc tttggaaaca gtcaagtgtt cttcacacta ctatagttta 780

aaactatatg attattggca tatactgact gactgcaata tttgtagtaa atagggaaaa 840
taagtattta gttggaggga taatttgatc gaatcacctg aatgttctat gtaatgtaaa 900
atattttttt cttgctttct tgtgttaagg tatatatctt atttgtatgg aattcttatt 960
caaatacagt tctattaaag agtatactcc tattggatga aaaaaaccta aaaaaaaaaa 1020
aaaaaaaaaa aaa                                     1033

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(2) INFORMATION ON SEQ ID NO. 124:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ICLLVHFVSR AKTVNLTFYSY WWVITENKDL FSCSLKSHK NNQIGSCLLS CVSWFLTCVH60
TPVCL 65

(2) INFORMATION ON SEQ ID NO. 125:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 64 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ISVFRLFKYL THFQTCTMEFY KPLDFQQHTI ENTCYSKHNF SVSSIAVVRD NIAISGMLQA60
FKIA 64

(2) INFORMATION ON SEQ ID NO. 126:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 61 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

KANLLPATPE GTQIWVGPFV QLGKRMGKPG DGFHKFSSGL WHSFQEIPLG KGLLANMHFQ60
T 61

(2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

LKNTNEVKAL NWYTLFTPIF QVWKCIFASR PLPRGISWKE CHNPLENLWK PSPGFPIRLP60
SWKTGPTHIW VPSGVAGRRF AF 82

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

HTWDOPYPLGI SPRTIRPVCQ PKVAFGMLNF PLSKKVHLPN EVTIRLNPCK SLDFVFYKNS60
TFPIKSLVIK ISTLPKCDST AWFLANKNPI 90

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

MVADYGCTIL ILGPFTHRNH TKWPDITYFE QFKYYTLAKS TYSTHPGEGG EKTHTYKTTS60
LDTMCLPTIS SLNNFHQLRC LV 82

(2) INFORMATION ON SEQ ID NO. 130:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 70 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

RNLVTQMKSG IEDPWTWQVN ADYSLAFPLY LCKEGYTELI LFQAYNFKFY HLNSSTFAAE60
EWNQKNVVSF 70

(2) INFORMATION ON SEQ ID NO. 131:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 60 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AIQCEAYFIA TLVDCQGDSA TVLDKLMFPF SLAANRRATY SAGSRARSWG SRGYTSSLII60

(2) INFORMATION ON SEQ ID NO. 132:

(i) SEQUENCE CHARACTERISTIC:


```

LSEDEIRTLK QKKIDETSEQ EOKHKETNNS NAQNPSEEEG EGQDEDILPL TLEEKENKEY 60
LKSLFEIIL MGKQNIPLDG HEADEIPEGL FTPDNFQALL ECRINSGEEV LRRKFETTAV120
NTLFCCKTQQ RQMLEICESC IREETLREVR DSHFFSIITD DVVDIAGEEH LPVLVRFVDE180
SHNLREEFIF FLPYEADAEI LAVKFHTMIT EKWGLNMEYC RGQAYIVSSG FSSKMKVVAS240
RLEKYPQAI YTLCCSCALN MWLAKSVPM GVSVALGTIE EVCSFFHRSP QLLLELDNVI300
AVLFQNSKER GKELKHCIS QWTGRHDAFE ILVELLQALV LCLDGINS DT NIRWNNYIAG360
RAFVLCSAVS DFDFIIVTVV LKNVLSFTRA FGKNLQGQTS DVFFAAGSLT AVLHSLNEVS420
GKY

```

(2) INFORMATION ON SEQ ID NO. 134:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

VENIEVYHEF WFEEATNLAT KLDIQMKLPG KFRRAHQGNL ESQLTSESYY KETLSVPTVE 60
 HIIQELKDIF SEQHLKALKC LSLVPSVMGQ LKENTSEHH ADMYRSDLPN PDTLSAELHC120
 WRIKWKHRGK DIELPSTIYE ALHLPDIKFF PNVYALLKVL CILPVMKVEN ERYENGRKRL180
 KAYLRNTLTD QRSSNLALLN INFEDIKHDLD LMVDYIKLY TSKSELPTDN SETVENT 237

(2) INFORMATION ON SEQ ID NO. 135:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

RIRINGSLCP QTKNNLYFHI VELSIGASV GERWYGMGES ILPARGESQG LLCLYFYKEI60
 LPLFLVNKLR GTDVGLEQGL SGGEGSWTA 89

(2) INFORMATION ON SEQ ID NO. 136:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 82 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(vi) ORIGIN
(A) ORGANISM: HUMAN

EEERAKREEL ERILEENNRRK IAEAQAKLAE EQLRIVEEQR KIHEERMKLE QERQRQQKEE60
OKIILGKGKS RPKLSFSLKT QD 82

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 71 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(vi) ORIGIN
(A) ORGANISM: HUMAN

SALKVEYLLS CPVSCRCVSS AAIRASFLFK MICTVSLAIP ASAAQPFIKK QHTRKAELRN60
ADVYGKKEQK M 71

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 67 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(vi) ORIGIN
(A) ORGANISM: HUMAN

SSAQRKYFNL PVEILVMERC QTVLNGRTSK SEATVPTRRG LLYCSTFSAL YFLAEASPWS60
AMYKLG 67

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

RAEKVEQYKS PRVVGTVASL LLVLPFKTVW HLSMTRISTG RLKYFLCAE

49

(2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

SCERRGFIMA DDLKRFLYKK LPSVEGLHAI VVSDRDGVPV IKVANDNAPE HALRPGFLST 60
 FALATDQGSK LGLSKNKSII CYYNTYQVVQ FNRLPLVVSF IASSSANTGL IVSLEKELAP120

LFEELRQVVE VS

132

(2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

QMILLFLESP SLLPWSVARA KVDKKPGRKA CSGALSFATL ITGTPSLSDT TMAWSPSTLG 60
NFLYKNRFRS SAMMNPLLSQ DQSPRLGFLG CLVLSAVTSG TALKTGSSSS HRHMIHDLVC120
APGSTF 126

(2) INFORMATION ON SEQ ID NO. 142:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 152 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

SAVKRGWDLN MAAVVAATAL KGRGARNARV LRGILAGATA NKASHNRTRA LQSHSSPEGK 60
EEPEPLSPEL EYIPRKRGN PMKAVGLAWA IGFP CGILLF ILTKREVDKD RVKQMKARQN120
MRLSNTGEYE SQRFRASSQS APSPDVGSGV QT 152

(2) INFORMATION ON SEQ ID NO. 143:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 114 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

EGRSAPQVCT PDPTSGDGAL WEEALNLWLS YSPVLDNRMF CRAFTCFTRS LSTSRLVRMK 60
RRIPQKGKMA QASPTAFMGF LPLFLGMYSS SGRGSGSSL PSGELWLCRA RVLL 114

(2) INFORMATION ON SEQ ID NO. 144:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 267 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

EDEVEEESTA LQKTDKKEIL KKSEKDTNSK VKPKGKVRWT GSRTGRWKY SSNDESESG 60
 SEKSSAASEE EEEKESEAI LADDDPCKK CGLPNHPELI LLCDSGSGY HTACLRPPLM120
 IIPDGEWFCP PCQHKLLCEK LEEQLQDLV ALKKKERAER RKERLVYVGI SIENIIPPQE180
 PDFSEDQEEK KKDSKKSKAN LLERRSTRTR KCISYRDEF DEAIDEAIED DIKEADGGGV240
 GRGKDSTIT GHRGKDISTI LDEKIIT 267

(2) INFORMATION ON SEQ ID NO. 145:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 185 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSSNFSQS SLOWQGGQNH 60
 SPSPGMIIRGG RRQAVWYPLS QESHRRISG WFGPHFLHG SSSSARMAS LSFSSSSSEA120
 ADDFSLPDPS LSSLLEYFEL PRVREPVHRT LPLGFTLEFV SFSDFFKISF LSVFCKAVDS180
 SSTSS 185

(2) INFORMATION ON SEQ ID NO. 148:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 134 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

KRQPTSAMKD PSRSSTSPSI INEDVIINGH SHEDDNPFAE YMWMENEEEF NRQIEEELWE 60
EEFIERCFQE MLEEEEEHEW FIPARDLPQT MDQIQDQFND LVISDGSSLE DLVVKSNLNP120
NAKEFVPGVK YGNI 134

(2) INFORMATION ON SEQ ID NO. 149:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 135 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

HSDKRAFTIK SSNTAFTVWK LCYIHQKRAP STQIFPYFTP GTNSFAFGFR LLLTTRSSRE 60
EPLITRSLN WSWIWSIVCG RSRAGINHSC SSSSSSISWK QRSINSSSHN SSSICLLNSS120
SFSIHMYSAN GLSSS 135

(2) INFORMATION ON SEQ ID NO. 150:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 58 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

LVSGANQCGS CNSKSFLTGA WYYRVGFRFF RGGLDFDFDF FFYVIFGKTH SELYLVT 58

(2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 61 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

FFVLKSLLVG ACYWEQVFVQ KLOSESLCIT ETLFITSLLS LPQKTVGLNK IICILYLYKC60
 L 61

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 60 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SACKFLRLDP LLTVDQLMYT CIKALNKSL WLITAKMGTR HLLCVLVTAV ALRAVRPCL160

(2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 56 amino acids

(B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

KRDIILNVFS QRSHKRKKNQ NQINHHEKNE TPHGNTKLWL GSSYYYSSHI GWRRKP 56

(2) INFORMATION ON SEQ ID NO. 155:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 150 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

IPVHRLHGSA DPLGWSIVSD LITSGLGAGV LRGLPARRLH SLGRRVLGRP GWLERLGHG 60
 RRDALGAWSA AQRPRTPGRP ACVCAPRRGP ESPSADPVPP PGRAGDPSPP DASASGPRGG120
 AATKAGPAHD PGQLRPELRV LPPPPRGDRE 150

(2) INFORMATION ON SEQ ID NO. 156:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 81 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

LPVAAGGRGQ DAQLRPELSG VVSRPRLGGG APSRSRGRI GVARVSSPAG RRDRVCGGGL60
 GASAGRAHAG GAARGAGPLR G 81

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 214 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

PGSQSVTPPM AEPLQPDPGA AEDAAAQAVE TPGWKAPEDA GPQPGSYEIR HYGPAKWVST 60
 SVESMDWDSA IQTGFTKLNS YIQGKNEKEM KIKMTAPVTS YVEPGSGPFS ESTITISLYI120
 PSEQQFDPPR PLESDVFIED RAEMTVFVRS FDGFSSAQKN QEQLLTLASI LREDGKVFDE180
 KVVYTAGYNS PVKLLNRNNE VWLIQKNEPT KENE 214

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

PNFYRGFIEN LTMCGGLSCL NLFRAVCSVH QMGRSGMGHL RPFRLSGLNRM LEPRLDSDL60
 RF 62

(2) INFORMATION ON SEQ ID NO. 159:

(i) SEQUENCE CHARACTERISTIC:

(A) ORGANISM: HUMAN

• • •

75

68

66

(A) LENGTH: 159 amino acids

```
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN
      (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:
```

(2) INFORMATION ON SEQ ID NO. 167:

(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```
EPVAQKSQLD RTVCISDAGA CGETLSVTSE ENSLVKKKER SLSSGSNFCS EQKTSGIINK240
FCSAKDSEHN EKYEDTFLES EEIGTKVEVV ERKEHLHTDI LKRGSEMDNN CSPTRKDFTE300
DTIPRNTSG RKTSLFYSSK YNKEALSPPR RKAFFKKWTPP RSPFNLVQET LFHDPWKKLLI360
ATILFLNRTSG KMAIPVLWKF LEKYPsAEVA RTADWRDVS E LLKPLGLYDL RAKTIVKFSD420
EYLTQWKYP IELHGIGAP
```

(2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

DCGKVQTMQ FALTNFLGLI SLCKTPVLSF LPQDRVQSFL KHALRCPLR HCFVDTLKGV60
 HKAKKSDQML RASNLYLTTW TWHWQKSLQH 90

(2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

SDFCQCHVQV VRYKLLALSI WSDFFALWTP LRVSTKQCLR CGHLRACFRK LCTLSCGRKE60
 RTGVLHKEIS PRKLVNANCI CVCTLPQSYI VF 92

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ADSHQNYIPW PPACVLLARP WLASLTREKD LQKIRLWDHF VCALGMTFFP TPGKPLGLSE60
TLWLANHMQS LKVERLSNPP IPREFQSVDV I 91

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 95 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

NGGLNAHLAS ASEFDHSGVQ LIEREEECICI FYEKINIQEK MKLNGEIEIH LLEEKIQFLK60
MKIAEKQRQI CVTQKLLPAK RSLDADLAVL QIQFS 95

(2) INFORMATION ON SEQ ID NO. 172:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 90 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

KTEFGAQLGR HPGTSQLAVI SGSHKEVFAS QQSSFSGIGS FLPVDVFQFL HLVSSSLGYL60
FFHKKCIPLL PALSAERHYG QIQRQLSGH 90

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

AVRSRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPIYA DKVRHPCFWT QSLYSDQLVL HMNFELICLST SA 102

(2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

VKRLCPKTRM PYLICINWNI MKWRYILSFL IFEEDSVLQG EGRGALLGAE AAHSAGVLPP60
 PLPQSHQPAR GAD 73

(2) INFORMATION ON SEQ ID NO. 175:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

RRQRKAEPGA CALGRVGSEC IPEPGARRTA QAAGLRVSG AANTKVRELK HFRFLGLLRS 60
 CRSEMEVDAP GVDGRDGLRE RRGFSEGGRO NFDVRPQSGA NGLPKHSYWL DLWLFILFDV120
 VVFLFVYFLP 130

(2) INFORMATION ON SEQ ID NO. 176:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ILKMATNFLN KEDRTLNRRI SHLQGTLPFI LHFVTNLQNS INWVGHPFL AKFLKLNPLV60
 RV 62

(2) INFORMATION ON SEQ ID NO. 177:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 174 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

AVYCILHQOK VLRLYKRALR HLESWCVQRO KYRYFACLMR ARFEEHKNEK DMAKATQLLK 60
 EAESEFWYRQ HPQPYIFPDS PGGTSYERYD CYKVPWCLOD DWHPSEKAMY PDYFAKREQW120
 KKLRAESWER EVKQLQEETP PGGPLTEALP PARKEGDLPP LWYIVTRPR ERPM 174

(2) INFORMATION ON SEQ ID NO. 178:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRMAV 60
DADGTRILPR PPSAAGWPSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVA?PAYKAA120
TPFADVVCNI R 131

(2) INFORMATION ON SEQ ID NO. 179:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SWSGVIPFF FSCSCLPFLY60
PPKWRQIHDL KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 180:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 140 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

KVLRKLIKPE EASQMAGAG PTMLLREENG CCSRRQSSSS AGDSGGERED SAAERARQQL 60
 EALLNKTMRI RMTDGRILVG CFLCTDRDCN VILGSAQEFL KPSDSFSAGE PRVLGLAMVP120
 GHHIVSIEVQ RESLTGPPYL 140

(2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SLKGKRHRGQ RYGGPVRLSL CTSMETMWCP GTMARPSTRG SPAEKESDGL RNSCAEPRMT 60
 LQSRVQRKQ PTSVRPSVMR MRIVLSSAS SCCRARSAAE SSRSPSESPA LELL 114

(2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

RLSRLTEPKE DPMAGISTAE HHLDPTAALP TQLSRSRHSP QVISTDGGET RGCGRQERKA60
 ERRVCKNAKV TFPVVGKQKQ RHWFOCHRQS EHLEL 95

(2) INFORMATION ON SEQ ID NO. 183:

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

DSRVYCFSGN YRKLVLPRKT GAIRNGSNIS KLRKQDVLSF AHLGFLLPF SLFSLRSLFQ60
FPSDLPLVPL ESQRL 75

(2) INFORMATION ON SEQ ID NO. 186:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 62 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

LGDSSEMPLL ALKCPVRLG TLEPSEILII LGSSPYFQMF SAQHWVLSST TENPEEKGR60
FP 62

(2) INFORMATION ON SEQ ID NO. 187:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 89 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

PHPSRRLTQG RWVRKSRVAM EKIPVSAFLR LVALSYNLAR DSTVKPGAKK DRKESRAKLR60
QTLRSRWGEQ LIWTQTYEEA LYKSRLATN 89

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GNPELPWRKF QCQHSICALWR SPTIWPGIAQ SNLEPKRTGR SLEPNCARPS PEVGVNNSSG60
LRRMKLYIN RD 72

(2) INFORMATION ON SEQ ID NO. 189:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

SLGHRPRNGG HSRGCDLGGL HAHSPDPRLO GAGLQAKNA AYSVSLPPGC VGHLWPHRL 60
HHRTGREHRA HTLLPLWDPL FHLLLLPAGS CCQSDQARPG EEAPFPVGDS GSGRGLQSP120
GCYRY 125

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```

RGRDSCFRSP PALRSSPAAL LRAGSSTKET ANALALGSRM ATTVPDGCNR GLKSKYYRLC 60
DKAEAWGIVL ETVATAGVVT SVAFMLTLPI LVCKVQDSNR RKMLPTQFLF LLGVLGIFGL120
TFAFIIGLDG STGPTRFFLF GILFSICFSC LLAHAVSLTK LVRGRKPLSR LVILGLAVGF180
SLVQDVIAIE YIVLTMNRTK                                     200

```

(2) INFORMATION ON SEQ ID NO. 191:

(i) **SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 111 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

AEAHGQTQNH QPGKGLPPPD ELGQTDMSQ QAGEADGKED PKEEEACGPC APVQSDDEGE 60
GEAKDAOHTO EEEKLSROHF SPVGVHLHAD EDRESEHEGH RGHNPGCGHR F 111

(2) INFORMATION ON SEQ ID NO. 192:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 92 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) **HYPOTHETICAL: yes**

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

EIWWETDYNH SGTIDAHEMR TALRKAGFTL NSQVQQTIAL RYACSKLGIN FDSFVACMIR60
 LETLFLKFLSL LDEKDKGMVQ LSLAEWLCCV LV 92

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ESLIAFLFLH DQCAQDSIVL TMIKDVVRIQ WTRNECKGGL EQRRGCPEGK ESYQILLNLQ60
PERLEFHRPQ SAPFHCSRHI K 81

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

KTTIHGPCQN HLPPPHCFK RPTLSKGDQ IDSSQEGFRA SIRAWPVLP LLSEQQGFQG60
SGWHESLSLP SCSEMTNVPR TQ 82

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

RPPPSRSSL AGQTNTQHS SARES

25

(2) INFORMATION ON SEQ ID NO. 196:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TMPSLSSRR LNSLKRVSR IIQATKLSKL MPSLLHAYRR AMVCCTWLLR VKPAFLRAVL60
ISWASMVPEW L

71

(2) INFORMATION ON SEQ ID NO. 197:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 86 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

IRRNTSRISV HTWRRTPPYD SPACFSCSIV SLESGFFSC VSVFFSFDLS NFSISAISGL60
SDMVAEEKQS EAHEYERQFL ASRRSG

86

(2) INFORMATION ON SEQ ID NO. 198:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

HPFSTFPTLP PQAGKFDATL LASQCILGGA RLLTIRLLAS PVQSFLWKAV DFSLASLSSS 60
VSTYRISRQ PYRVCQTWLR RKSKARTST SDSSRLAAV A 101

(2) INFORMATION ON SEQ ID NO. 199:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 100 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TPFPSPQLYP LKQVNSTQHF SHLSAYLAH ASLRFACLL LFNRFPGRW IFLRLCLLQ 60
FRLIEFLDLS HIGFVRHGCG GKAKRGARVR ATVPRVSPQW 100

(2) INFORMATION ON SEQ ID NO. 200:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 153 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GLTDQYLELN ALQEELGPFG LVILGFPSNQ FGKQEPGENS EILPSLK YVR PGGGFVPNFQ 60
 LFEKGOVNGE KEQKFYTFK NSCPPTAELL GSPGRLEWEP MKIHDIRWNF EKFLVGPDI120
 PVMRWYHRTT VSNVKMDILS YMRRQAALSA RGK 153

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 249 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

LMPPPYPYPL PIMQGPRRGS SGRKPHSQSF YPHPRFSFLL HKRQAWHNCV SEPLWTRDNC 60
 PSVCMATQPR ICLLETQGWS ICVYGLAQHP HIFFSFLFQM SPKETQVLGP MVLLKPEHHS120
 WGQHLPHAHT THHQPPSSFL KDPPEPPSPS HSAPETSQDN CERDGRVPQV RGGVSMKEGP180
 EALVGGPPLS PSVVPALSAF RLRLPGRDTT PAPLEDMLSS HSVHWYLNTP ICPVKVFLQQ240
 KKKRKKKKK 249

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 156 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGLSAPFPAP LLCRAQAPLA LGPNFSYRHG VRPGSSPGAH LPEARCGGGP RGRSQAQSPQ 60
 SSGPVGGGRGR SGSKARTPQL FRLQQQLQRF GHGCEVPRCW LQAAREHPGQ GQEAQSEEEG120
 EGQEGEGQEE GGSPLKGPQ GSLNLPCLR VPTTWS 156

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 113 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

DPTSLTAMEF DLGAALEPTS QKPGVGAGHG GDPKLSPHKV QGRSEAGAGP GPKQGHSSS 60
 DSSSSSSDSD TDVKSHAAGS KQHESIPGKA KKPVKKKKEK GKKEKGKKKE APH 113

(2) INFORMATION ON SEQ ID NO. 204:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 162 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

GGPPPPKHLs SRWLVLVGRE EGLMSPVQGP SVGSLLLLLAL LLLALLLLH FGLLGLARDA 60
 LVLLGASSVG LHIRVRIAGA AAGVGRAVVS LLWTRTCPCL RPALNFVGTG LGISPVARPH120
 TGLLGGGLQG CSQVELHGGK RSWVLRPRAP GPCRGAEQGE ER 162

(2) INFORMATION ON SEQ ID NO. 205:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 145 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

VEPWTTTCRAA GAVMADYWKS QPKKFCDYCK CWIADNRPSV EFHERGKNHK ENVAKRISEI 60
KQKSLDKAKE EEKASKEFAA MEAAALKAYQ EDLKRGLGES EILEPSITPV TSTIPPTSTS120
NQQKEKKEKK KKRSEFKGQMG RRHNL 145

(2) INFORMATION ON SEQ ID NO. 206:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 262 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

PALSHLPRHQ INRKKRKRRR KKDPKGRWV EGITSEGYHY YYDLISGASQ WEKPEGFQGD 60
LKKTAVKTVW VEGLSEDGFT YYNTETGES RWEKPDDFIP HTSDLPSSKV NENSLGTLDE120
SKSSDSHSDS DGEQAEIEGG VSTETEKPKI KFKEKNKNSD GGSDPETQKE KSIQKQNSLG180
SNEEKSKTLK KSNPYGEWQE IKQEVESHEE VDLELPSTEN EYVSTSEADG GGEPKVVFE240
KTVTSLGVMA DGVAPVFKKR RT 262

(2) INFORMATION ON SEQ ID NO. 207:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 73 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GKGRRKGIKG VCCNGGSCPE SIPRGFEKTW LRVRNFGAKH NTSNQHYPTY LDIKSTERKE60
REEEKKILQR ADG 73

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

IWNFQALKMS MYQLQKLMVA ENPKWYLKKK QSLLELWQM EWPQSSKREE LENGKILGKF60
KGNEVMIQ 68

(2) INFORMATION ON SEQ ID NO. 210:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 194 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SVHCFREDKM KFTIVFAGLL GVFLAPALAN YNINVNDNN NAGSGQQSVS VNNEHNVANV 60
DNNNGWDSWN SIWDYGNGFA ATRLFQKTC IVHKMNKEVM PSIQSLDALV KEKKLQGKGP120
GGPPPKGLMY SVNPNKVDDL SKFGKNIANM CRGIPTYMAE EMQEASLFFY SGTCYTTSVL130
WIVDISFCGD TVEN 194

(2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VHQALGRWSS WSLTLKLLFL DQCIKGLNGG HDFLVHVFVN ACLLLKESGC SKAISIIPDG60
 IPGVPSVVIV NIGHIVFIVD TH 82

(2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ELGLNHLWLR VWLEPTAQVP DVLFPFEMER EEKAVSLLLW FNVKEPQLPP LPGREAFGFL 60
 LLLLALVAGE VLQDHRLLAQ LVLAGLRAHA GRLRFRKALT KASARCAPEG WTSESFASF 119

(2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

IICGCVSGLS PLHRSLMYCF QSSWRGRKRL YLCCSGLMSK SRSSLLCLAE KPLAFFFFSL 60
RLWRVKYSRT TALRCWSRR ACGLMRGVCA SGRPSRRPRP AVLLKAGHRS HSPLSETMHG120
RSHSSFSDRF RRSLMT 136

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 101 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TLETVHQGPV QWAQARHAAT DDSGQALKGR SSRGYFSDK IQMPLLCGYR RNPSTGNKAH 60
FQNYHQRRPP ESYPOAKLRV HCGNRWLYFL HLREQIPASV K 101

(2) INFORMATION ON SEQ ID NO. 215:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 204 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LRCPAFRSTA GRGLREGLPE AQTPRMSPQA REDQLQRKAV VLEYFTRHKKR KEKKKKAKGF 60
 SARQRRELRL FDIKPEQQRY SLFLPLHELW KQYIRDLCSSG LKPDTPQPMI QAKLLKADLH120
 GAIISVTKSK CPSYVGITGI LLQETKHIFK IITKEDRLKV IPKLNCVFTV ETDGFISYIY180
 GSKFQLRSSE RSARKFKAKG TIDL 204

(2) INFORMATION ON SEQ ID NO. 216:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 645 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

PTRPVAAGSE QQQQSAFIQE RQPVALMRLI SFNVPHIKNS TGEPIWKVLI YDRFGQDIIS 60
 PLLSVKELRD MGITLHLLH SDRDPIPDVP AVYFVMPTEE NIDRMCQDLR NQLYESYYLN120
 FISAISSKL EDIANAALAA SAVTQVAKVF DQYLNFILE DDMFVLCNQK KELVSYRAIN180
 RPDITTEME TVMDTIVDSL FCFFVTLGAV PIIRCSRGTA AEMVAVKLDK KLRENLRDAR240
 NSLFTGDTLG AGQFSFQRPL LVLVDRNIDL ATPLHHTWTY QALVHDVLDL HLNVRNLEES300
 SGVENSPAGA RPKRKNKKS YDLTPVDKFWQ KHKGSPPFEV AESVQQELES YRAQEDEVKR360
 LKSIMGLEGE DEGAISMLSD NTAKLTSAVS SLPELLEKKR LIDLHTNVAT AVLEHIKARK420
 LDVYFEYEEK IMSKTTLDKS LLDIISDPDA GTPEDKMRLF LIYYISTQQA PSEADLEQYK480
 KALTDAGCNL NPLQYIKQWK AFTKMASAPA SYGSTTTKPM GLLSRVMNTG SQFVMEGVKN540
 LVLKQQNLVP TRILDNLMM KSNPETDDYR YFDPKMLRGN DSSVPRNKNP FQEAIVFVVG600
 GGNYYIEQNL VDYIKGKQKG HILYGCSELF NATQFIKQLS QLGQK 645

(2) INFORMATION ON SEQ ID NO. 217:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GAGPSQLRLH YPRISMAVRQ WVIALALAA LVDREVPA AGKLPFSRMP ICEHVMESPT 60
 CSQMSNLVCG TDGLTYTNEC QLCLARIKTK QDIQIMKDGK C 101

(2) INFORMATION ON SEQ ID NO. 218:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

QLGWIFYFMS YPLHAHHCSP ADTSWLEVLL WDQHLPSFMI WMSCLVFIRA KQSWHSFVYV 60
 SPSVPQTRLD IWEQVGDDSTM CSQMGIKLG SFPATGTSL STTRRAAKAR AITHWRTAML120
 ILG 123

(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 64 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

IKAKENLNAF FFFFLLRSEI GTVILSTERQ TIKWAMKGGG KVLIVRGIQ PEIKPIYKHV60
 CSSK 64

(2) INFORMATION ON SEQ ID NO. 220:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 67 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

SFAIPFPWHC TISPIIGQSL GFLGFTMVAT TIRLIDGSNL KKKVMVMDKI SRSREVCYHK60
ITVASTS 67

(2) INFORMATION ON SEQ ID NO. 221:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 117 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

TIISITDSQ LOEVAEQLEI FAALHEVLHI INDRKNLKGQ LOEVAEQLEL ERIGPQHQAQ 60
SDSLTGMAF FKMREFFED HIDDAKYCGH LYGLGSGSSY VQNGTGNAYE EEANKQS 117

(2) INFORMATION ON SEQ ID NO. 222:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 196 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

PTCPIQHFIM MKLWVPSRSL PNSPNHYRSF LSHTLHIRYN NSLFISNTHL SRRKLRVTNP 60
IYTRKRSINI FYLLIPSCRT RLILWIIYIY RNLKHWSTST VRSHSHSIYR LRPSMRTNII120
LRCHSYKPP ISHPYWNPN SRMNLRLLS RQSHLDPILR FPLHLTIYYR GPSNRSPLP180
PRNRIKQPNR IKLRCR 196

(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 174 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

LPSAIEGPTP VSALLHSSTI VVAGIFLLVR FHPLTNNNF ILTTILCLGA LTTLFTAICA 60
 LTQNDIKKII AFSTSSQLGL IIVTLGINQP HLAFLHICHT AFFKAILFIC SGSIHSLAD120
 EQDIRKIGNI TKIIPFTSSC LVIGSLALTG IPFLTGFYSK DLIIEAINTC NTNA 174

(2) INFORMATION ON SEQ ID NO. 224:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

FLKTTALIIS VLGFLIALEL NNLTIKLSIN KANPYSSFST LGFFPSIIH RITPIKSLNL 60
 SLKTSLTLLD LIWLEKTIPK STSTLHTNIT TLTTNQKGLI KLYFISFLIN IILIIILYSI120
 NLE 123

(2) INFORMATION ON SEQ ID NO. 225:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 129 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

NMLLAEVRIS MVIRNSVRYL MNRLMFGSEC IYHEENCIID HVTKRATDVN RIEKKSVLKL 60
ILSSIEFMVT QCQVVIYSI LLWKNINRGK RLIMKENLID VVVYSGKLMC LIRFDIEIRI120
GDSRRMKIK 129

(2) INFORMATION ON SEQ ID NO. 226:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

FFFFFFFAIQ MNVYFLNPHR VRAELRDAWH SISHPGSLPR SFFFAGSILD LYHFLQRQYP60
EWQSQVYFKV GVFSGSRGDW IPS 83

(2) INFORMATION ON SEQ ID NO. 227:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 122 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

SMMLFKVLVI TVFCGLTVAF PLSELVSINK ELQNSIIDLL NSVFDQLGSY RGTKAPLEDY 60
 TDDDLSTDSE QIMDFTPAAN KQNSEFSTDV ETVSSGFLEE FTENTDITVK IPLAGNPVSP120
 TS 122

(2) INFORMATION ON SEQ ID NO. 228:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

TSTTVFFFPF HSLPVGCTV CSHALCINIL EIYRSVLYFL YCWILIIKTF TRVLNKSSLT60
 RK 62

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ARPCMNSTKA LPHGREHTRL KMLSYLKNKM CKSSGWHKTK VNASWGTF LR GLAECVNIID60
 FCLOYMTSVT SLKICTIQFQ LWITSVDLCE GFYLCRMGV 99

(2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

GELQKSSHYH PPFLFEMIFF VHFGCSIGGR IYYNMDHLYF CIYLFITRPQ PQSSFSPSTS60
LCL 63

(2) INFORMATION ON SEQ ID NO. 231:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 64 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

INKYRSRDDP YYSIFYHQYC SQNVQKKSEF ITQEDDNGWT FVIHLKDCGR ANSTHCIVCA60
YGGL 64

(2) INFORMATION ON SEQ ID NO. 232:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 88 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

PLFCAILKTC TFYFSDSLTF LIECVLYHAV MLWYYSYRVL PILKTCHEPK RSFDSALEVL60
HKLKSLSNIN MKGGTGCNIY SQVTSLYI 88

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(2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

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ASTIMDLLFG RRTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIAD IKKMAKQGQM 60
DAVRIMAKDL VRTRYVRKF VLMRANIQAV SLKIOTLKSNS NSMAQAMKGV TKAMGTMNRQ120
LKLPIQKIM MEFERQAEIM DMKEERIELL HLMIPWVLGK F 161
  
```

(2) INFORMATION ON SEQ ID NO. 234:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

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RRVRTKSFAM MRTASIWPCL AIFLMSAMIF FSWVSSFCRS RSSSRMARFR ALWFCRSSSS 60
GVFRRPNNRS MMVEAHWQAG AGTDTRFRFR VTLLFLGSPT CPPTKAPRSC RRRRRFRGRV120
  
```

(2) INFORMATION ON SEQ ID NO. 235:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

KLPQNPRDHQ MQQFNPLLLH IHDLCPLPLK HHDLDDLGLQL QLSVHGAGHL GDTLHGLCHR 60
VVGLECLDLE GHSLDVGP HQ YKLAHIAPGA HQVFCHDANS IHLALLGHLL NVCNDFLLLG120
L 121

(2) INFORMATION ON SEQ ID NO. 236:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 180 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

KTKRSVKDAA KKGQKDVCI V LAKEMIRSRK AVSKLYASKA HMNSVLMGMK NQLAVLRVAG 60
SLQKSTEV MK AMQSLVKIPE IQATMRELSK EMMKAGIIEE MLEDTFESMD DQEEMEEAE120
MEIDRILFEI TAGALGKAPS KVTDALPEPE PPGAMAASED EGEEEEEAL EA MQSRLATLRS180

(2) INFORMATION ON SEQ ID NO. 237:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 111 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

LMPFQSQNLQ ERWLPQMRG RKRRLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60
ALHLCCEDYH FGEGSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRKKKK K 111

(2) INFORMATION ON SEQ ID NO. 238:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 103 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

KICERCCQEG PEGCLHSSGQ GDDQVKEGCE QAVCIQSTHE LSAHGDEEPA RGLASGWFFA 60
 EEHRSDDEGHA KSCEDSRDSG HHEGVVQRND EGWDHRGDVR GHF 103

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 351 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

TWCTTTMLAA RLVCLRTLPS RVFHFAFTKA SPVVKNSITK NQWLLTPSRE YATKTRIGIR 60
 RGRGQELKE AALEPSMEKI FKIDQMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIEKAV120
 IWPQYVKDRI HSTYMYLAGS IGLTALSAIA ISRTPVLMNF MMRGSWVTIG VTFAAMVGAG180
 MLVRSIPYDQ SPGPKHLAWL LHSGVMGAVV APLTILGGPL LIRAAWYTAG IVGGLSTVAM240
 CAPSEKFLNM GAPLGVGLGL VEVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFSMFLLYD300
 TQKVIKRAEV SPMYGVQKYD PINSMLSIYM DTLNIFMRVA TMLATGGNRK K 351

(2) INFORMATION ON SEQ ID NO. 240:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

RVAPATVVG RNI DPNEDTK TRPRPTPRGA PMFRNFSLGA HMATVERPPT MPAVYHAALM 60
RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120
MKFMRTGVLL IAMADKAVKP ILPAKYI 147

(2) INFORMATION ON SEQ ID NO. 241:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 196 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

KARRRGTMAA AADERSPEDG EDEEEEEQLV LVELSGIIDS DFLSKCENKC KVLGIDTERP 60
ILQVDSCVFA GEYEDTLGTC VIFEENVEHA DTEGNNKTVL KYKCHTMKKL SMTRTLLTEK120
KEGEENIGGV EWLQIKDNDF SYRPNMICNF LHENEDEEVV ASAPDKSLEL EEEEIQMNHR180
FKPGFVEPGE PIAPWE 196

(2) INFORMATION ON SEQ ID NO. 242:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 156 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PPAPALRHRE TRRPVASLHV GTGALGARSH PPAGSRHLEF WQKQFARRGA DGQEPNKLLR 60
 LGAEARTQDG GSGRAWPVTR RRGAA GPWRR RRTSGVQRTE KTRKRRSSWF WWNYQELLIQ120
 TSSQNVKINA RFWALTLRGP FCKWTA VSL L GSMKTL 156

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 132 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

RRLEVS YRQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEYQSL 60
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLLKYE FDIEFDIPIT YPTTAPEIAV120
 PELDGKTAKM YR 132

(2) INFORMATION ON SEQ ID NO. 244:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 159 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

LFAISYSVLP VHLCCLSIQL RNCNFWGSSR ICDRNVKLDV KLIFQEVMDI PAFSKPPSSF 60
 LVGLQSEPIV VSILVVLHIP DKGLIFLLQS LHPQLTISGS GVS LQHRDLR HNTSRGFIRH120
 LGPGRKRNAE VVLPVAYLKA PSSLLWEDET LGCCKTSFE 159

(2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATLPDALPPA TKFFLKAFDD SLPSPIQSYL YIFAVFPSSS GTAISGAVVG YVIGMSNSMS 60
 NSYFRRSWIY QHFPNHRVPS LLDSSRNQSL SAFLLFSTYR IRD 103

(2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 285 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPIYA DKDVFHVVVE VPRWSNAKME IATKDPLNPI KQDVKKGKLR YVANLFPYKG120
 YIWNYGAIPO TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180
 GETDWKVIAI NVDDPDAANY NDINDVKRLK PGYLEATVDW FFRYKVPDGG PENEFAFNAE240
 FKDKDFAIDI IKSTHDHWKA LVTKKTNGKR IMLIVQLFVG PLKVC 285

(2) INFORMATION ON SEQ ID NO. 247:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

TKGLRIAQAQ LCPGSPRCRS QSISRRACAL CLRPSTQPNT TYLRKPGGRK RAVGHKSPAE60
TRVPASVQRS QPPRAHRKSC LASLGLCKNN KCLS 94

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 113 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

DPRPSRIQHI SGNPAGASER LAIRAQLKRE YLLQYNDPNR RGLIENPALL RWAYARTINV 60
YPNFRPTPKN SLMGALCGFG PLIFIYYIHK TERDRKEKLI QEGKLDRTFH LSY 113

(2) INFORMATION ON SEQ ID NO. 249:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 98 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

VFRSGSEIRI DIYCSCIGPT KQGRIFDEPS AVGIVVLKQV LSFQLGSYGQ PLACARRVSG60
DMLYSAGSRV SGRVRRLDGL YFGNDILANQ GTIAPARF 98

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

SKGCSITETV TVDPGSIIP LGLTQYRRGA VVFTLKHTFL SDGFRNLRV VTTSVKGPLN 60
LRSVGGSRT R ICSSSPWPLR RTPSERQRR GGGLLAGGG RWREGRGSEF ASLLFLVRLC120
STTELCWOIC FOIDE 135

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 189 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) **HYPOTHETICAL: yes**

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```

SMQSAVSFFF FSLDQKKICL PTISLVVWPT VTIFLCVQRH IGFAENDLLR LENTIKTNCS 60
ATGQVYYYYQI ITSRCQLHIE SFMKFINKEL FFLCGFNKSS RIVQSLVNVI LIIPLNFICC120
CYLLKYDLFR LLIPLIQEMP RGIPWNGAS YSVNFSSFTF ANIMAEFFLS LVRQLLTEFF180
LTIILSHGI

```

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 300 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```

KSIWKQICQH  KNVVEQSLTR  KRRDANSPL  PSRHRPPPPA  SKPPPALRCL  SDGVRLRGHG  60
EDEQILVLDP  PTDLKFKGPF  TDVVTNNKL  RNPSPDRKVC  KVKTTAPRRY  CVRPNSGIID  120
PGSTVTVSVM  LQPFYDQDPN  KSKHKFMVQT  IFAPNTSDM   EAVWKEAKPD  ELMQSKLRCV  180
FEMPENNDKL  NDMEPSKAVP  LNASQDQDGM  PKPHSVSLND  TETRKLMEEC  KRLQEGEMMK  240
SEENRHLRDE  GLRLRKVAHS  DKPGSTSTAS  FRDNVTSPLP  SLLVIAAIF  IGFGLGKFIL  300

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[illegible]

(2) INFORMATION ON SEQ ID NO. 255:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 247 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSLK HEDKRGGSGS 60
 HNWGTVKDEL TESPXYIQKQ ISYNYSDLQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120
 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSKSE EAHAEVSVMD180
 HHFRKPANDI TSQLEINFGD LGRPGRGGRG GRGGRGRGGR PNRGSRTDKS SASAPDVDDP240
 EAFPALA 247

(2) INFORMATION ON SEQ ID NO. 256:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 69 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

FVFDSSPVVR SATSTFVLVL QARSITSTMP IKFTFATRIK SISSAHSTST APSTLFQDHH60
 DLESRAARA 69

(2) INFORMATION ON SEQ ID NO. 257:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 220 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(vi) ORIGIN
(A) ORGANISM: HUMAN

PGRGSMYDRM RRGGDGYDGG YGGFDDYGGY NNYGYGNDGF DDRMRDGRGM GGHGYGGAGD 60
 ASSGFHGGHF VHMRLPLFRA TENDIANFFS PLNPIRVHID IGADGRATGE ADVEFVTHED120
 AVAAMSKDKN NMQHRYIELF LNSTPGGGSG MGGSGMGGYG RDGMNDQGGY GSVGRMGMCN180
 NYSGGYGTPO GGGYGRGGG GSGGYYGOGG MSGGGWRGMY 220

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1105 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| AATGAGCCTG | GTGTTAGATG | AGTTTTACAG | CTCACTCAGG | GTGGTGGGTG | TCTCTGCTGT | 60 |
| TCTGGGTACT | GGATTAGATG | AACTCTTTGT | GCAAGTTACC | AGTGCTGCCG | AAGAATATGA | 120 |
| AAGGGAGTAT | CGTCCTGAAT | ATGAACGTCT | GAAAAAATCA | CTGGCCAACG | CAGAGAGCCA | 180 |
| ACAGCAGAGA | GAACAACCTG | AACGCCTTCG | AAAAGATATG | GGTTCGTAG | CCTTGGATGC | 240 |
| AGGGACTCCC | AAAGACAGCT | TATCTCCTGT | GCTGCACCTT | TCTGATTGA | TCCTGACTCG | 300 |
| ACCAACATTG | GAAGCAGACA | CGGATATCTA | TGCACCTTAC | CAGAGGTGA | CAGAGGAAAG | 360 |
| CCATGAAGAG | CGAGCATTCC | AGAATTTTAT | GCAAGAATCG | ATGGCACAAT | ACTGGAAGAG | 420 |
| AAACAATAAA | TAGGAGACTT | TAGCACACTT | CACTTGTTTC | TAGAAGTCCA | GAATTTTGA | 480 |
| CCTCCACGTG | AAAGAACTGT | TCTTACCTCT | GAAGTGGGGG | CTCCATAAG | GGATAATTTT | 540 |
| CCTCAGAGTA | GCAAAGTTTC | TCTTATTAGA | GAAATCTTGT | GACTCAGATG | AAGTCAGGGA | 600 |
| TAGAAGACCC | TTGGACCTGG | CAGGTTAATG | CTGATTATTC | CTTGGCCTTT | CCCTTGTATT | 660 |
| TATGCAAGGA | AGGATAATACT | GAGCTGATAC | TCTTCCAAGC | CTACAACCTC | AAGTTTTATC | 720 |
| ATTTGAACCT | AGTACTTTTT | GCTGCTGAGG | AATGGAATCA | AAAGAACGTA | GTCTCTCTGT | 780 |
| AACCACTCA | GATCTCTATT | ATTAGGCTAG | ATGTATAGCC | TCTACTCCCC | CAGCTTCTTG | 840 |
| CTCTTGACCC | TGCACTGTAA | GTTGCCCTTC | TATTAGCAGC | CAAGGAAAAG | GGAAACATGA | 900 |
| GCTTATCCAG | AACGGTGGCA | GAGTCTCCTT | GGCAATCAAC | CAACGTTGCT | ATGAAATATG | 960 |
| CCTCACACTG | TATAGCTCAT | TATAGGACGT | CAGGTTTGTT | GAAAAAAGTG | GGCAAGACAT | 1020 |
| GATTAATGAA | TCAGAAATCCT | GTTTCATTGG | TGACTTGATG | AAAGACTTTT | TAATTTTAAA | 1080 |
| AAAAA | AAAAA | AAAAA | | | | 1105 |

(2) INFORMATION ON SEQ ID NO. 259:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

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ATTCCAAACA TGGCGGCTCC ACTAGGGGGT ATGTTTTCTG GGCAGCCACC CGGTCCCCCT 60
CAGGCCCCGC CGGGCCTTCC GGGCCAAGCT TCGCTTCTTC AGGCAGCTCC AGGCGCTCCT 120
AGACCTTCCA GCAGTACTTT GGTGGACGAG TTGGAGTCAT CTTTCGAGGC TTGCTTTGCA 180
TCTCTGGTGA GTCAGGACTA TGTCAATGGC ACCGATCAGG AAGAAATTCG AACCGGTGTT 240
GATCAGTGTA TCCAGAAGTT TCTGGATATT GCAAGACAGA CAGAATGTTT TTTCTTACAA 300
AAAAGATTGC AGTTATCTGT CCAGAAACCA GAGCAAGTTA TCAAAGAGGA TGTGTCAGAA 360
CTAAGGAATG AATTACAGCG GAAAGATGCA CTAGTCCAGA AGCACTTGAC AAAGCTGAGG 420
CATTGGCAGC AGGTGCTGGA GGACATCAAC GTGCAGCACA AAAAGCCCCG CGACATCCCT 480
CAGGGCTCCT TGGCCTACCT GGAGCAGGCA TCTGCCAACA TCCCTGCACC TCTGAAGCCA 540
ACGTGAGCAA AGGGCAGAGG CAGTTGGCCT ATGAGTGGGC TGATGCGTGA GGTGGGCCAC 600
ACATTCCCTC CTGTGGACTT GACATTTTGG AAGAACTCTT TGCCAGATAA TGAGTTCATT 660
TTAGTTTTAT GCTCCCATTG AAAAATTTTC CACTATTTTT ATAAGCTGTT AATTTCTTGA 720
GTACTTTATA ACATGTCTGT AGCTTGATAA AACCAAGTAA GTATTTTTTT TTTGTCTTTA 780
GCGAAGTTTA GACTGTGAAT ATGATGACAC AGATTCTTTT TTATGGTGGC TTTGCTTGTT 840
TTAAATTTTT GCATGACTTT TCATCTTTTT ATGTGTGTTT CCTGTAGTTT GATCCGAAGG 900
AAAAGAGTAT AGTAGCCTGA GAATCAGGAG ATGGGAGTTT TAGTCGTAGG CCTTATGATA 960
ATTACCCCGC GGTGGTGTGT AGAAAAGTAT GTAAATTTGC TCTGTTTTAA GACTTTGAAC 1020
TACCTCAAGA AGAGGAATCT AATACAATAT TTGTAATGTT AAAAAAAAAA AAAAAAAAAA 1080
AAAAAAAAA

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(2) INFORMATION ON SEQ ID NO. 260:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3292 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

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ATGCCGAAC TCTGCGCTGC CCCCACCTGC ACGCGGAAGA GCACGCAGTC CGACTTGGCC 60
TTCTTCAGGT TCCGCGGGGA CCCTGCCAGA TGCCAGAAGT GGGTGGAGAA CTGTAGGAGA 120
GCAGACTTAG AAGATAAAAC ACCTGATCAG CTAAATAAAC ATTATCGATT ATGTGCCAAA 180
CATTTTGAGA CCTCTATGAT CTGTAGAACT AGTCCTTATA GGACAGTTCT TCGAGATAAT 240
GCAATACCAA CAATATTTGA TCTTACCAGT CATTTGAACA ACCCACATAG TAGACACAGA 300
AAACGAATAA AAGAACTGAG TGAAGATGAA ATCAGGACAC TGAAACAGAA AAAAATTGAT 360
GAAACTTCTG AGCAGGAACA AAAACATAAA GAAACCAACA ATAGCAATGC TCAGAACCCC 420
AGCGAAGAAG AGGGTGAAGG GCAAGATGAG GACATTTTAC CTCTAACCC TGAAGAGAAG 480
GAAAACAAAG AATACCTAAA ATCTCTATTT GAAATCTTGA TTCTGATGGG AAAGCAAAAC 540
ATACCTCTGG ATGGACATGA GGCTGATGAA ATCCCAGAAG GTCTCTTTAC TCCAGATAAC 600
TTTCAGGCAC TGCTGGAGTG TCGGATAAAT TCTGGTGAAG AGGTTCTGAG AAAGCGGTTT 660
GAGACAACAG CAGTTAACAC GTTGTTTTGT TCAAAAACAC AGCAGAGGCA GATGCTAGAG 720
ATCTGTGAGA GCTGTATTGG AGAAGAAACT CTCAGGGAAG TGAGAGACTC ACACCTCTTT 780
TCCATTATCA CTGACGATGT AGTGGACATA GCAGGGGAAG AGCACCTACC TGTGTTGGTG 840
AGGTTTGTG ATGAATCTCA TAACCTAAGA GAGGAATTTA TAGGCTTCCT GCCTTATGAA 900
GCCGATGCAG AAATTTTGGC TGTGAAATTT CACACTATGA TAACTGAGAA GTGGGGATTA 960
AATATGGAGT ATTGTCGTGG CCAGGCTTAC ATTGTCTCTA GTGGATTTTC TTCCAAATG1020
AAAGTTGTTG CTTCTAGACT TTTAGAGAAA TATCCCCAAG CTATCTACAC ACTCTGCTCT1080
TCCTGTGCC TAAATATGTG GTTGGCAAAA TCAGTACCTG TTATGGGAGT ATCTGTTGCA1140
TTAGGAACAA TTGAGGAAGT TTGTTCTTTT TTCCATCNGA TCACCACAAC TGCTTTTAGA1200
ACTTGACAAC GTAATTGCTG TTCTTTTCA GAACAGTAAA GAAAGGGGTA AAGAACTGAA1260
GGAAATCTGC CATTCTCAGT GGACAGGCAG GCATGATGCT TTTGAAATTT TAGTGGAACT1320
CCTGCAAGCA CTTGTTTTAT GTTTAGATGG TATAAATAGT GACACAAATA TTAGNATGGG1380
AATAACTATA TAGCTGGCCG AGCATTNGT ACTCTGCAGT GCAGTGCAG ATTTTGATTT1440
CATTGTTACT ATTGTTGTTC TTAATAATGT CCTATCTTTT ACAAGAGCCT TTGGGAAAAA1500
CCTNCCANGG GGCAACCTC GTGATGTCTT CTTTGGCGCC GGTAGCTTGA CTNGCAGTAC1560
TGNNCATTCA CNTCAACGAA GTGAGTGGGA AAATATTNGA AGTTATCAT GAATTTTGGT1620
TTGAGGAAGC CACAAATTTG GCAACCAAAC TTGATATTCA AATGAAACTC CCTGGGAAAT1680
TCCGCAGAGC TCACCNNAGG GTAACCTGGA ATCTCAGCTA ACNCTCTGAG AGTTACTATA1740
AAGAAACCCN TAAGTGTCCC AACAGTGGAG CACATTATTC AGGAACCTAA AGATATATTC1800
TCAGAACAGC ACCTCAAAGC TCTTAAATGC TTATCTCTGG TACCCTCAGT CATGGGACAA1860
CTCAAATTCA ATACGNTCNG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA1920
ATCCTGACAC GCTGTCAGCT GAGCTTCATT GTTGGAGAAT CAAATGGAAA CACAGGGGGA1980
AAGATATAGA GCTTCCGTCC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTT2040
TTCTTAATGT GTATGCATTG CTGAAGGTCC TGTGTATTCT TCCTGTGATG AAGGTTGAGA2100
ATGAGCGGTA TGAAATGGN ACGAAAGCGT CTTTAAAGCA TATTTGAGGG AACACTTTGA2160
CAGACCCAAA GGTCAAGTAA CTTGGCTTTT GCTTTAACAT AAATTTTGGA TATTTAAACA2220
CGACCTGGAT TTAATGGTGG ACACATATAT TAAACTCTAT ACAAGTAAGT CAGAGCTTCC2280
TACAGATAAT TCCGAAACTG TGGNAAAATA CCTAAGAGAC TTTTAAAAAT AGGCTTCTT2340
ATATTTGATA TTTGGAAGAA AAAGCCGTAA GGTGTATGTA GACCACTTAA TCACTAAATA2400
TCTTTGCCNA TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTTAAATGG2460
CCCCTGTTG AACTCTCAAG CTTTGAAGAC CTACCTGTTT TTCCAGAAGA GAACGTTGAA2520
AGTGCCATGT TTCCNTTTTG CGTGATCTCT GTTGATGGCA CTCTGGAATT GTTTCAGTTA2580
AGTCATTTTA GACATAGCAT TTATTATCAC TGTGGNATCT CTAATTGTTG GGTGTTATGA2640
ATTCTTTGNA AGNAAATATA TTTTNGAAGA GGTGTGGGNA GGNAAGGAAT ACNATTTTAT2700
NAAAATGTTG TAGTGNAAGN CCCACAATTN GACCTTTNGA CTAATANGGA GTTTTAAGTA2760
TNGTTAAAAA TNCTATACTG GNNACAGNTT ACAAGAAATT ACCGGAGAAA AGCTTGTGAG2820
CTCACCNAAA CAAGGNATTT NCAGTGTAGA TTTTGTCTNT TCTTGAACNT TNAAAGAAAN2880
CAAATGANCA AAGTTTGAAT NGGAAAAGCC TGCTGTTGTT CCNACATCTC NGTTGCTGTT2940
NNTACANTTC CNNTTTGTG GAGNCCTACN ATCTTNCCTA AGCTTTTTNA GCANGGTATA3000

TNGTTGAACA CTCTCTGTTT CATGGTTGAG ACAGAATCAG AGGCCATGGA TACTGACAAC3060
TGATTGTCT GTTTTTTTT TCTGTCTTTN TTCCATGACT CTTATATACT GCCTCATCTT3120
GATTTATAAG CNAAAANCCT GGANAAACCT ANCAAAATAA GTGTTGTGGT TTATCTAGAA3180
AAATATGGAA AATATTGCTG TTATTTTGG TGAAGAAAT CNAATTTTGT ATAGTTTATT3240
TCAATCTAAA TAAAATGTGA ATTTTGTTTA AAAAAAAAAA AAAAAAAAAA AA 3292

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(2) INFORMATION ON SEQ ID NO. 261:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1196 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

GGTAGAAAAT GCAATAAATT CTGGGACAAT GCCCAGACCT CTGGCATAGA GGAGCCTTCT 60
GAGACAAAGG GTTCTATGCA AAAAAGCAAA TTCAAATATA AGTTGGTTCC TGAAGAAGAA 120
ACCACTGCCT CAGAAAATAC AGAGATAACC TCTGAAAGGC AGAAAGAGGG CATCAAATTA 180
ACAATCAGGA TATCAAGTCG GAAAAAGAAG CCCGATTCTC CCCCCAAAGT TCTAGAACCA 240
GAAAACAAGC AAGAGAAGAC AGAAAAGGAA GAGGAGAAAA CAAATGTGGG TCGTACTTTA 300
AGAAGATCTC CAAGAAATATC TAGACCCACT GCAAAAGTGG CTGAGATCAG AGATCAGAAA 360
GCTGATAAAA AAAGAGGGGA AGGAGAAGAT GAGGTGGAAG AAGAGTCAAC AGCTTTGCAA 420
AAAAGTGACA AAAAGGAAAT TTTGAAAAAA TCAGAGAAAG ATACAAATTC TAAAGTAAGC 480
AAGGTAAAAA CCAAAGGCAA AGTTTCGATGG ACTGGTTCTC GGACACGTGG CAGATGGAAA 540
TATTCCAGCA ATGATGAAAG TGAAGGGTCT GGCAGTGAAA AATCATCTGC AGCTTCAGAA 600
GAGGAGGAAG AAAAGGAAAG TGAAGAAGCC ATCCTAGCAG ATGATGATGA ACCATGCAAA 660
AAATGTGGCC TTCAAACCA TCCTGAGCTA ATTCTTCTGT GTGACTCTTG CGATAGTGGA 720
TACCATACTG CCTGCCTTCG CCCTCCTCTG ATGATCATCC CAGATGGAGA ATGGTTCTGC 780
CCACCTTGCC AACATAAACT GCTCTGTGAA AAATTAGAGG AACAGTTGCA GGATTTGGAT 840
GTTGCCTTAA AGAAGAAAGA GCGTGCCGAA CGAAGAAAAG AACGCTTGGT GTATGTTGGT 900
ATCAGTATTG AAAACATCAT TCCTCCACAA GAGCCAGACT TTTCTGAAGA TCAAGAAGAA 960
AAGAAAAAAG ATTCAAAAAA ATCCAAAGCA AACTTGCTTG AAAGGAGGTC AACAAGAACA1020
AGGAAATGTA TAAGCTACAG ATTTGATGAG TTTGATGAAG CAATTGATGA AGCTATTGAA1080
GATGACATCA AAGAAGCCGA TGGAGGAGGA GTTGGCCGAG GAAAAGATAT CTCCACCATC1140
ACAGGTCATC GTGGGAAGA CATCTCTACT ATTTTGGATG AAAAAATAAT AACGGC 1196

```

(2) INFORMATION ON SEQ ID NO. 262:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

AAGGACGCTT GCCTTTTTC GGTGCGGGAA GGGGGAAGAA GGTAACCTCC GGTGACGGGG 60
TTGCATCACT TCCTCTCAAG CTGCGGCGTT TGTGTTGGTGG GGTACACGC GGGTTCAACA 120
TGCCTATCGA AAAGTGTTAT TTCTGTTCCG GGGCCATCTA TCCTGGACAC GGCATGATGT 180
TCGTCCGCAA CGATTGCAAG GTGTTGAGAT TTTGCAAATC TAAATGTCAT AAAAAGCTTTA 240
AAAAGAAGCG CAATCCTCGC AAAGTTAGGT GGACCAAAGC ATTCCGGAAA GCAGCTGGTA 300
AAGAGCTTAC AGTGGATAAT TCATTTGAAT TTGAAAAACG TAGAAATGAA CCTATCAAAT 360
ACCAGCGAGA GCTATGGAAT AAAACTATTG ATGCGATGAA GAGAGTTGAA GAAATCAAAC 420
AGAAGCGCCA AGCTAAATTT ATAATGAACA GATTGAAGAA AAATAAAGAG CTACAGAAAG 480
TTCAGGATAT CAAAGAAGTC AAGCAAAACA TCCATCTTAT CCGAGCCCCT CTTGCAGGCA 540
AAGGGAACA GTTGAAGAG AAAATGGTAC AGCAGTTACA AGAGGATGTG GACATGGAAG 600
ATGCTCCTTA AAAATCTCTG TAACCATTTT TTTTATGTAC ATTTGAAAAT GCCCTTTGGA 660
TACTTGGAAC TGCTAAATTA TTTTATTTTT TACATAAGGT CACTTAAATG AAAAGCGATT 720
AAAAGACATC TTTCTGTCAT TGCCATCTAC ATAATATCAG ATATTACGGA TGTTAGATTG 780
CATCTCAGTG TTAAATCTTT ACTGATAGAT GTACTTAAGT AAATCATGAA AATTCTACTT 840
GTAACATAG AAGTGAATTG TGGACGTAAA ATGGTTGTGC TATTTGGATA ATGGCACTAG 900
GCAGCATTTG TATAGTAACT AATGGCAAAA ATTCATGGCT AGTGATGTAT AAAATAAAAT 960
ATTCCTTTGCA GTAAAATATT CCCTTTGTTA ATGTTATAGA AGGGGGGATA CAAAAAGGAA1020
CTAACAATTT GTATGGCAGT GTCAGATATT TTTATTTTAG TATTTCTGT TTTGGTTTAT1080
TTGCATCTTA GAAGAGCATA ATGACATTGT TTGATGAAGC CTAATTATGC TGGACTGTTT1140
TGACCTGGTT TAACCCTTCT GATAGGTAGT TGTGGATGCT GGGGATGAGA ACTGAATAAT1200
CTTTGCCTGG AGTGACACTA CACTCTAGAA TTTCCACTTT GGAGAATACT CAGTTCCAAC1260
TTGTGATTCC TGATAGAACA GACTTTACTT TTCTAGCCCA GCATTGATCT AGAAGCAGAG1320
GAATCCCAGC GCCTTTTAAA AGTTGTTATG TGGTTTTCTT TAAAAAGCT CCTGTTTTTG1380
AAAAGTAGAA TTTATGGGTA CAACGTATGT TCATTATTTG TACATAAAAT AAAACCATTT1440
AAAAAGTAAA AAAAAAATAA AAAAAAC
1467

```

(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 739 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

CGGCTCGAGC CCGGCTCAGT CACCCGCAGC AGGCGTGCAG TTTCCCGGCT CTCCGCGCGG 60
CCGGGGAAGG TCAGCGCCGT AATGGCGTTC TTGGCGTCGG GACCCTACCT GACCCATCAG120
CAAAAGGTGT TGCGGCTTTA TAAGCGGGCG CTACGCCACC TCGAGTCGTG GTGCGTCCAG180
AGAGACAAAT ACCGATACTT TGCTTGTTTG ATGAGAGCCC GGTTTGAAGA ACATAAGAAT240
GAAAAGGATA TGGCGAAGGC CACCCAGCTG CTGAAGGAGG CCGAGGAAGA ATTCTGGTAC300
CGTCAGCATC CACAGCCATA CATCTTCCCT GACTCTCCTG GGGGCACCTC CTATGAGAGA360
TACGATTGCT ACAAGGTCCC AGAATGGTGC TTAGATGACT GGCATCCTTC TGAGAAGGCA420
ATGTATCCTG ATTACTTTGC CAAGAGAGAA CAGTGGAAGA AACTGCGGAG GGAAAGCTGG480
GAACGAGAGG TTAAGCAGCT GCAGGAGGAA ACGCCACCTG GTGGTCCTTT AACTGAAGCT540
TTGCCCCCTG CCGGAAAGGA AGGTGATTTG CCCCCACTGT GGTGGTATAT TGTGACCAGA600
CCCCGGGAGC GGCCCATGTA GAAAGAGAGA GACCTCATCT TTCATGCTTG CAAGTGAAAT660
ATGTTACAGA ACATGCACTT GCCCTAATAA AAAATCAGTG AAATGGAAAA AAAAAAAAAA720
AAAAAAAAAA AAAAAAAAAA

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739

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2146 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| TTTTTTTTTT | TTTTTTTTTT | TCCCAGGCCG | TCTTTTTTATT | TACAGTGATA | CCAAACCATC | 60 |
| CACCTGCAAA | TTCTTTGGTC | TCCCATCAGC | TGGAATTAAAG | TAGGTACTGT | GTATCTTTGA | 120 |
| GATCATGTAT | TTGTCTCCAC | CTTGGTGGAT | ACAAGAAAGG | AAGGCACGAA | CAGCTGAAAA | 180 |
| AGAAGGGTAT | CACACCGCTC | CAGCTGGAAT | CCAGCAGGAA | CCTCTGAGCA | TGCCACAGCT | 240 |
| GAACACTTAA | AAGAGGAAAG | AAGGACAGCT | GCTCTTCATT | TATTTTGAAA | GCAAATTCAT | 300 |
| TTGAAAGTGC | ATAAATGGTC | ATCATAAGTC | AAACGTATCA | ATTAGACCTT | CAACCTAGGC | 360 |
| TATTTAATAA | TACACCACAC | TGAAATTATT | TGCCAATGAA | TCCCAAAGAT | TTGGTACAAA | 420 |
| TAGTACAATT | CGTATTGGCT | TTCCTCTTTT | CTTCTCTCAG | ACAAACACCA | AATAAAATGC | 480 |
| AGGTGAAAG | GATGAACCA | CGCTAGAGGC | TGACTTAGAA | ATTTATGCTG | ACTCGATCTA | 540 |
| AAAAAAATTA | TGTTGGTTAA | CGTTAACCTA | TCTAAAATCG | GGCCCTTTTCG | GCAAGCCCTT | 600 |
| CAAAGGAGGT | CAAGTCACAG | TCATACAGCT | AGAAAAGTCC | CTGAAAAAAA | GAATTGTTAA | 660 |
| GAAGTATAAT | AACCTTTTCA | AAACCCACAA | CGCAGCTTAG | TTTTCTTTTA | TTTATTGTGTG | 720 |
| GTCATGAAGA | CTATCCCCAT | TTCTCCATAA | AACCTCTCCT | CCATACGTCT | GCATTATGGC | 780 |
| ACAAAAGACT | CTAAGTGCCA | CCAGACAGAA | GGACCAGAGT | TTCGATTAT | AAACAATGAT | 840 |
| GCTGGGTAAT | GCTTTAAATGA | GAACATTGGA | TATGGATGGT | CAGATGAAAG | CTCGAGCCGA | 900 |
| ATTCCGGTCTG | AGTTTTCATC | TGACCATCCA | TATCCAATGT | TCTCATTTAA | ACATTACCCA | 960 |
| GCATCATTGT | TTATAATCAG | AAACTCTGGT | CCTTCTGTCT | GGTGGCACTT | AGAGTCTTTT | 1020 |
| GTGCCATAAT | GCAGCAGTAT | GGAGGGAGGA | TTTTATGGAG | AAATGGGGAT | AGTCTTCATG | 1080 |
| ACCACAAATA | AATAAAGGAA | AACTAAGCTG | CATTGTGGGT | TTTGAAAAGG | TTATTATACT | 1140 |
| TCTTAACAAT | TCTTTTTTCA | GGGACTTTTC | TAGCTGTATG | ACTGTTACTT | AAACTATCTA | 1200 |
| AAATAGAGCA | TTTTGGTATC | TTTCACTCTG | CCATCCATAT | CCAATGTTCT | CATTTAAACA | 1260 |
| TTACCCAGCA | TCATTGTTTA | TAATCAGAAA | CTCTGGTCCT | TCTGTCTGGT | GGCACTTAGA | 1320 |
| GTCTTTTGTG | CCATAATGCA | GCAGTATGGA | GGGAGGATTT | TATGGAGAAA | TGGGGATAGT | 1380 |
| CTTCATGACC | ACAAATAAAT | AAAGGAAAAC | TAAGCTGCAT | TGTGGGTTTT | GAAAAGGTTA | 1440 |
| TTATACTTCT | TAACAATTCT | TTTTTTCAGG | GACTTTTTCTA | GCTGTATGAC | TGTTAGTTGA | 1500 |
| CCTTCTTTGA | AAAGCATTCC | CAAAATGCTC | TATTTTATAG | AGATTAACAT | TAACCAACAT | 1560 |
| AATTTTTTTT | AGATCGAGTC | AGCATAAAAT | TCTAAGTCAG | CCTCTAGTCG | TGGTTCATCT | 1620 |
| CTTTCACCTG | CATTTTATTT | GGTGTGTTG | TGAAGAAAGG | AAAGAGGAAA | GCAAAACGA | 1680 |
| ATTGTACTAT | TTGTACCAAA | TCTTTGGGAT | TCATTGGCAA | ATAATTTTCAG | TGTGGTGTAT | 1740 |
| TATTAATAG | AAAAAAAAAA | TTTTGTTTCC | TAGGTTGAAG | GTCTAATTGA | TACGTTTGAC | 1800 |
| TTATGATGAC | CATTTATGCA | CTTTCAAAAT | AATTTGCTTT | CAAAATAAAT | GAAGAGCAGC | 1860 |
| TGTCCTTCTT | TCCTCTTTTA | AGTGTTTCAG | TGTGGCATGC | TCAGAGGTTT | CTGCTGGATT | 1920 |
| CCAGCTGGAG | CGGTGTGATA | CCCTCTTTTT | TCAGCTGTTT | GTGCCTTCCT | TTCTTGATCT | 1980 |
| CACCAAGATG | GAGACAAATA | CATGATCTCA | AAGATACACA | GTACCTACTT | AATTCCAGCT | 2040 |
| GATGGGAGAC | CAAGAATTTT | GCAAGTGGAT | GGTTTGGTAT | CACCTGTAAT | AAAAAGAGGG | 2100 |
| CCTGGGAATT | CTTGCGATT | CATCTCTAAA | AAAAAAAAAA | AAAAAA | | 2146 |

(2) INFORMATION ON SEQ ID NO. 265:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```

CAAGTAAATG CAGCACTAGT GGGTGGGATT GAGGCTATGC CCTGGTGCAT AAATAGAGAC 60
TCAGCTGTGC TGGCACACTC AGCGGCTCTG GACCGCATCC TAGCCGCCGA CTCACACAAG 120
GCAGGTGGGT GAGGAAATCC AGAGTTGCCA TGGAGAAAAT TCCAGTGTCA GCATTCTTGC 180
TCCTTGTTGGC CCTCTCCTAC ACTCTGGCCA GAGATACCAC AGTCAAACCT GGAGCCAAAA 240
AGGACACAAA GGACTCTCGA CCCAACTGC CCCAGACCCT CTCCAGAGGT TGGGGTGACC 300
AACTCATCTG GACTCAGACA TATGAAGAAG CTCTATATAA ATCCAAGACA AGCAACAAAC 360
CCTTGATGAT TATTCATCAC TTGGATGAGT GCCCACACAG TCAAGCTTTA AAGAAAGTGT 420
TTGCTGAAAA TAAAGAAATC CAGAAATTGG CAGAGCAGTT TGTCTCTCTC AATCTGGTTT 480
ATGAAACAAC TGACAAACAC CTTTCTCCTG ATGGCCAGTA TGTCCCCAGG ATTATGTTTG 540
TTGACCCATC TCTGACAGTT AGAGCCGATA TCACTGGAAG ATATTCAAAC CGTCTCTATG 600
CTTACGAACC TGCAGATACA GCTCTGTTGC TTGACAACAT GAAGAAAGCT CTCAGTTGTC 660
TGAAGACTGA ATTGTAAAGA AAAAAAATCT CCAAGCCCTT CTGTCTGTCA GGCCTTGAGA 720
CTTGAAACCA GAAGAAGTGT GAGAAGACTG GCTAGTGTGG AAGCATAGTG AACACACTGA 780
TTAGGTTATG GTTTAATGTT ACAACAATA TTTTAAAGA AAAACAAGTT TTAGAAATTT 840
GGTTTCAAGT GTACATGTGT GAAAACAATA TTGTATACTA CCATAGTGAG CCATGATTTT 900
CTAAAAAAA AAATAAATGT TTTGGGGGTG TTCTGTTTTC TCCAAAAAAA AAAAAAAA 960
AAAAAAA AAAAATAATGCC CCCAAGGGGA CGGGTTACAA TTGGGGGGCG1020

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(2) INFORMATION ON SEQ ID NO. 266:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1652 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

AATTCGGATC CATGGGCCAC AGTGGATGGC TTGAAATGTG GCTGAGCGCT TCGGACAATT 60
CGGATCCATG NNNNGTGGCC ACCCCAAGAC GCGCCCCAGC CCGCCATGGC CCGGATCCTN 120
NCCGGGNNTC CTGCCTTCTG TCCCTGCTCC TGGCCGGNGT TTGTTCCGCC GGGCCGGGGA 180
CAAGAGAAGT CTAAGACAGA CTGCCATGGC GGTNATGAGT GGTACCATCT ACGAGTATGG 240
AGCCCTCACC ATCGATGGGG AGGAATACAT TCCTTTTAAG CAGTATGCAG GCAAATATAT 300
CCTCTTTGTC AACGTAGCCA GCTACTGAGG TCTGACAGAC CAATACCTTG AACTGAATGC 360
ACTACAAGAA GAACTTGGGC CATTTGGCTN TGGTCATTCT GGGCTTCCCT TCCAACCAAT 420
TTGGCAAACA GGAGCCAGGC GAGAACTCGG AGATACTCCC CAGTCTCAAG TATGTTGNN 480
ACCAGGTNNG GGGGCTTTGT GNCCTAATTN NNTTCCAGNC TCNTTTGAGA AANNGGANGA 540

TNGTNGAACN GGGGAGNAAA GAGCNAGAAA TTCTACACTT TCCTGAAGAA CTCCTGCCCT 600
CCCCTGCGAG NAACTCCTGG GNCTCANCCT GCGCCGNCCTC TTTTGGGAAC CCATGAAGAT 660
CCATGACATN CCGCTGGAAC TTTGAGAAGT TCCTGGTNGG GGCCNAGANT GGCATACCGG 720
TTATGCGCTG GTACACCGG ACCACAGTCN AGCAACGTCN AAGATGGACA TCCTGNTCNT 780
TACATGAGGC GGCAGGCANG CCCTGANGCG CCNAGGGGGN AAGTAACTGA NTGCCNNNC 840
CACCTACCC CTACCCCTG CCCATCATNG CAAGGGCCGA NGGAGGGGCT CTNCAGGAA 900
GGAAGCCACA TTCCCAGTCA TTCTNANCCC CCACCCCAAGA TTCTCTTNC TTNATTACAT 960
AAAAGACAAG CCNTGGCACA ACTGTGTGTC TGAACCACTG TNGGACACGT GACAATTGTN1020
CCCAGTGTGT GCATGGCTAC ACAGNCCACG TATCTGCCTG CNTTGAAACC CANGGGNATG1080
GTCCATCNTG TNGTTTACGG NCTTGGCACA ACACCCNNTC ATATTTTTTT CAGCNTTTCT1140
GTTCCAAANN TGAGNNCCCA AANNGGAAAC ACNAANGTTC TNAGGTCCNA ATNGGTTCTG1200
CTCAAANCCN TGANACATNC ATTCNTGGG GNCCANGCAT CNTCCACAT NGCCACACN1260
TACACACCAC CNAGCCTCCT TCTTCTTNC CTGNAAGGAC CCNTCCNNNN TGAGCCCCCA1320
AGCCNCATCC CACAGTGCNT CCTGAGACCA GCCAAGACAA CTGTGAGCGC GATGGCCGTG1380
TANCCCCAGG TNCAGGGGNT GGTGTCTCTA TGAAGGANNG GGNNCCCGNA AGCCCTGTN1440
GGGNCGGNGC CTCCCCTGAG CCCNGTCTGT GGTGCCNAGC CCTTAGTGCA TTCAGGCTTA1500
GGCTCCCNAG GCANGGGACA CTACCCCGC GCCTCTGGAG GACATGCTAT CCTCTACTC1560
TGTCCACTGG TATCTCAACA CCCCCATCTG CCCAGTAAAG GTCTTTCTGC AGCAAAAAAA1620
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA GG 1652

```

(2) INFORMATION ON SEQ ID NO. 267:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

GGAGTGGCCC TCTGTGAGGG GCTCAAATGG TTGCAATTCA TGGCGCGTTA CGACTTGGCT 60
CACTTAATCA AATCCCTACC AACTCTAACT TGCCGAAGGA AGAACTTGAC CTCTTGGAGA 120
ACCCTCGATT GGTTTTTCCT GCCATTTAGA TGTTGAAGTA CCCCATGAAG AGCTGCAAAA 180
ATTCTCAAAG GTGGATTACA GGAGGTGGCA GAACAGTTAG AGCTGGAACG GATAGGACCA 240
CAACATCAGG CAGGATCTGA TTCATTGCTC ACAGGAATGG CCTTTTCAA AATGAGAGAA 300
ATGTTCTTTG AAGATCATAT TGATGATGCC AAATATTGTG GTCATTGTA TGGCCTTGGT 360
TCTGGTTCAT CCTATGTACA GAATGGCACA GGAATGCAT ATGAAGAGGA AGCCAACAAG 420
CAGTCATGAC ATGAAATAGT CCTTTTATTT TTATTTTCGAG CTACACACAT GCTTGTATAT 480
AGGTTTTATC TCTGGTTGAA TCCCTCGAAC AATAGACAGT ACCTTTCCCC CCCCTTTCAT 540
GGCCCATTTT ATTGTCTGCC TTTCAGTACT AAGTATGACC GTTCCTATCT CAGATCTTAA 600
TAAAAAGAAA AAAAAAAGCG CATTGAGGTT AAATTTGGCC TTAATTTAAT ATACTTGTTA 660
GCAAGCGTGT GTGACAGAGA GTGGGGGAAAG CTACATCATT GAATATTTTG ATAAACTTTA 720
CCGACTTGAG TTTGGTTTAT TTTTCCCTTT TCCTAAATTA ACTAGCACTG ACTGTAATTT 780

ATTTCCTGT TTCACGTCTC TCCCTTCCAT TCTGCAGGAG TTTTAGCTAT TTGAGATCGT 840
GGACCATCAG TTTTGCACCT TAGAGAGTGT TTCTGACTCT AAACCTGTTT TATCAGAAAA 900
TTTGTTTTTT CTGTATCTTA GCTGGAAAAA TCTGCCAACT TTACACAGTA TTTACTTGGT 960
TTTGACCCAC AGAATATAGC ACGTTGTGCA AACTGTGCGT TCAGCGAAAC TTAAGAAAGA 1020
CAAGAACTA CTGAGGAGCT TAGTAAGTGC TGTCTCTGTA CGTAGTGTTT AATCTTCCAA 1080
GCACATCTAG TGTCTGTCAG TTTCTAATTG GCATGTGTAG GCTGCTCTGT GACTGAAGAA 1140
TTTTCAAACC AGCTTTACAC CCTTCAGGAA AAATCCCTGT GATTGGATGG TTACTATCTG 1200
CCAGGAACTG GTACCCAGAT GTGAAGCACA GTTATTATGA TAGACACTTC CTGAGTGCTA 1260
TTGTATCCAC ACCATTACCT TTTTTTTTAA ATTGGAGCCA TCTATGAGCC TGATTGTGGT 1320
CGCAACCATT GTAAAACCCA GAAAGCCTAG GGATTGGCCA ATAATTGGGG AAATGGTGCA 1380
GTGCCAAGGA AATGGGATGG CAAAAGAAG

```

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

| | | | | | | |
|-------------|------------|-------------|------------|-------------|------------|-----|
| CCACGCGTC | CCGGAACGG | CGGCGCGGC | GACAGGACG | AGGGGCTTA | GTTGGTGGGC | 60 |
| AAGTCGGGGA | TCCAGAAAG | AGAAGCGTGA | CCCGGAAGCG | GAAACGGGTG | TCCGTCCCAG | 120 |
| CTCCGGCCTG | CCAGTGA | TCTACCATGA | TGGACCTATT | GTTCGGGCGC | CGGAAGACGC | 180 |
| CAGAGGAGCT | ACTGCGGCAG | AACCAGAGGG | CCCTGAACCG | TGCCATGCGG | GAGCTGGACC | 240 |
| CGGAGCGACA | GAAACTAGAG | ACCCAGGAGA | AGAAAAATCT | TGCAGACATT | AAGAAGATGG | 300 |
| CCAAGCAAGG | CCAGATGGAT | GCTGTTTCGCA | TCATGGCAA | AGACTTGGTG | CGCACCCGGC | 360 |
| GCTATGTGCG | CAAGTTTGTA | TTGATGCGGG | CCAACATCCA | GGCTGTGTCC | CTCAAGATCC | 420 |
| AGACACTCAA | GTCCAACAAC | TCGATGGCAC | AAGCCATGAA | GGGTGTCA | AAGGCCATGG | 480 |
| GCACCATCAA | CAGACAGCTG | AAGTTGCCCC | AGATCCAGAA | GATCATGATG | GAGTTTGA | 540 |
| GGCAGGCAGA | GATCATGGAT | ATGAAGGAGA | AGATGATGAA | TGATGCCATT | GATGATCCCA | 600 |
| TGGGTGATGA | GGAAGATGAA | GAGGAGAGTG | ATGCTGTGGT | GTCCCAGGTT | CTGGATGAGC | 660 |
| TGGGACTTAG | CCTAACAGAT | GAGCTGTCTGA | ACCTCCCCTC | AAC TGGGGGC | TCGCTTAGTG | 720 |
| TGGCTGTGTG | TGGGAAAAAA | GCAGGCGCCG | CAGCCTCAGC | CCTAGCTGAT | GCTGTGCAG | 780 |
| ACCTGGAGTA | ACGGCTTAAG | AACCTGCGGA | GGGACTGAGT | GGCCCTGCCA | CTCCGAGATA | 840 |
| ACCAAGTGGAT | GCCCAAGATC | TTTTACCACA | ACCCCTCTGT | AATAAAAGAG | ATTTGACACT | 900 |

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1145 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

GGGCCCCGCC CAGGCGGCTG CCCGTGACCT GCCTGGGCGC GGGGAAGTGA AAGCCGGAAG 60
GGGCAAGACG GGTTCAGTTC GTCATGGGGC TGTTTGGAAA GACCCAGGAG AAGCCGCCCA 120
AAGAACTGGT CAATGAGTGG TCATTGAAGA TAAGAAAGGA AATGAGAGTT GTTGACAGGC 180
AAATAAGGGA TATCCAAAGA GAAGAAGAAA AAGTGAAACG ATCTGTGAAA GATGCTGCCA 240
AGAAGGGCCA GAAGGATGTC TGCATAGTTC TGGCCAAGGA GATGATCAGG TCAAGGAAGG 300
CTGTGAGCAA GCTGTATGCA TCCAAAGCAC ACATGAACTC AGTGCTCATG GGGATGAAGA 360
ACCAGCTCGC GGTCTTGCGA GTGGCTGGTT CCCTGCAGAA GAGCACAGAA GTGATGAAGG 420
CCATGCAAAG TCTTGTGAAG ATTCCAGAGA TTCAGGCCAC CATGAGGGAG TTGTCCAAAG 480
AAATGATGAA GGCTGGGATC ATAGAGGAGA TGTTAGAGGA CACTTTTGAA AGCATGGACG 540
ATCAGGAAGA AATGGAGGAA GAAGCAGAAA TGGAAATTGA CAGAATTCTC TTTGAAATTA 600
CAGCAGGGGC CTTGGGCAAA GCACCCAGTA AAGTGAAGTGA TGCCCTTCCA GAGCCAGAAC 660
CTCCAGGAGC GATGGCTGCC TCAGAGGATG AGGGGGAGGA GGAAGAGGCT CTGGAGGCCA 720
TGCAGTCCCG GCTGGCCACA CTCCGCAGCT AGGGGCTGCC TACCCCGCTG GGTGTGCAC 780
CACTCCTCTC AAGAGCTGCC ATTTTATGTG TCTCTGAC TACACCTCTG TTGTGAGGAC 840
TACCATTTTG GAGAAGGTTT TGTGTGCTC TTTTCATTCT CTGCCCAGGT TTTGGGATCG 900
CAAAGGGATT GTTCTTATAA AAGTGGCATA AATAAATGCA TCATTTTATG GAGTATAGAC 960
AGATATATCT TATTGTGGGG AGGGGAAAGA AATCCATCTG CTCATGAAGC ACTTCTGAAA1020
ATATAGGTGA TTGCCTGAAT GTCGAAGACT CTACTTTTGT CTATAAAACA CTATATAAAT1080
GAATTTTAAT AAATTTTTCG TTTAGCACTT GGCCCCATTG TAGATTGCC TGTGCAGTAA1140
ACTTT
1145

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(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1836 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

GTTGCGACAT GCAGTGCGCC GGAGGAACTG TGCTCTTTGA GGCCGACGCT AGGGGCCCCGG 60
AAGGGAAACT GCGAGGCGAA GGTGACCGGG GACCGAGCAT TTCAGATCTG CTCGGTAGAC 120
CTGGTGCAAC ACCACCATGT TGGCTGCAAG GCTGGTGTGT CTCCGGACAC TACCTTCTAG 180
GGTTTTCCAC CCAGCTTTCA CCAAGGCCTC CCCTGTTGTG AAGAATTCCA TCACGAAGAA 240
TCAATGGCTG TTAACACCTA GCAGGGAATA TGCCACCAAA ACAAGAATTG GGATCCGGCG 300
TGGGAGAACT GGCCAAGAAC TCAAAGAGGC AGCATTGGAA CCATCGATGG AAAAAATATT 360
TAAATTTGAT CAGATGGGAA GATGGTTTGT TGCTGGAGGG GCTGCTGTTG GTCTTGGAGC 420
ATTGTGCTAC TATGGCTTGG GACTGTCTAA TGAGATTGGA GCTATTGAAA AGGCTGTAAT 480
TTGGCCTCAG TATGTCAAGG ATAGAATTCA TTCCACCTAT ATGTACTTAG CAGGGAGTAT 540
TGGTTTAAAC GCTTTGTCTG CCATAGCAAT CAGCAGAACG CCTGTTCTCA TGAACCTCAT 600
GATGAGAGGC TCTTGGGTGA CAATTGGTGT GACCTTTGCA GCCATGGTTG GAGCTGGAAT 660
GCTGGTACGA TCAATACCAT ATGACCAGAG CCCAGGCCCA AAGCATCTTG CTTGGTTGCT 720
ACATTCTGGT GTGATGGGTG CAGTGGTGGC TCCTCTGACA ATATTAGGGG GTCCTCTTCT 780
CATCAGAGCT GCATGGTACA CAGCTGGCAT TGTGGGAGGC CTCTCCACTG TGGCCATGTG 840
TGCGCCCACT GAAAAGTTTC TGAACATGGG TGCACCCCTG GGAGTGGGCC TGGGTCTCGT 900
CTTTGTGTCC TCATTGGGAT CTATGTTTCT TCCACCTACC ACCGTGGCTG GTGCCACTCT 960
TTACTCAGTG GCAATGTACG GTGGATTAGT TCTTTTCAGC ATGTTCCCTT TGTATGATAC1020
CCAGAAAGTA ATCAAGCGTG CAGAAGTATC ACCAATGTAT GGAGTTCAAA AATATGATCC1080
CATTAACTCG ATGCTGAGTA TCTACATGGA TACATTAAAT ATATTTATGC GAGTTGCAAC1140
TATGCTGGCA ACTGGAGGCA ACAGAAAGAA ATGAAGTGAC TCAGCTTCTG GCTTCTCTGC1200
TACATCAAAAT ATCTTGTTTA ATGGGGCAGA TATGCATTAA ATAGTTTGTA CAAGCAGCTT1260
TCGTTGAAGT TTAGAAGATA AGAAACATGT CATCATATTT AAATGTTCCG GTAATGTGAT1320
GCCTCAGGTC TGCCTTTTTT TCTGGAGAAT AAATGCAGTA ATCCTCTCCC AAATAAGCAC1380
ACACATTTTC AATTCTCATG TTTGAGTGAT TTTAAATGT TTTGGTGAAT GTGAAAATA1440
AAGTTTGTGT CATGAGAATG TAAGTCTTTT TTCTACTTTA AAATTTAGTA GGTTCAGTGA1500
GTAACAAAAA TTTAGCAAAC CTGTGTTTGC ATATTTTTTT GGAGTGCAGA ATATTGTAAT1560
TAATGTCATA AGTGATTTGG AGCTTTGGTA AAGGGACCAG AGAGAAGGAG TCACCTGCAG1620
TCTTTTGTTT TTTTAAATAC TTAGAACTTA GCACCTGTGT TATTGATTAG TGAGGAGCCA1680
GTAAGAAACA TCTGGGTATT TGGAAACAAG TGGTCATTGG TTACATTCAT CTGCTGAACT1740
TAACAAAACT GGTTCCATCC TGGAACAGGG CACAGGTGAA TGCATTCTCT CTGCGGTTGG1800
CTCCCCAGTG GCGCGCCTTC CCATATAGGA TGTGGG 1836

```

(2) INFORMATION ON SEQ ID NO. 271:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1220 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

1220

(2) INFORMATION ON SEQ ID NO. 272:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1303 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) **ORIGIN:**

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

CGCAGTGCGC AGGCGTGGGG CTCTCTCCTT GTCAGTCGGC GCCGCGTGCG GGCTGGTGGC 60
TCTGTGGCAG CGGCGGCGGC AGGACTCCGG CACTATGAGC GGCTTCAGCA CCGAGGAGCG 120
CGCCGCGCCC TTCTCCCTGG AGTACCGAGT CTTCCTCAA AATGAGAAAG GACAATATAT 180
ATCTCCATTT CATGATATTC CAATTTATGC AGATAAGGAT GTGTTTCACA TGGTAGTTGA 240
AGTACCACGC TGGTCTAATG CAAAAATGGA GATTGCTACA AAGGACCCTT TAAACCCTAT 300
TAAACAAGAT GTGAAAAAAG GAAACTTCG CTATGTTGCG AATTTGTTCC CGTATAAAGG 360
ATATATCTGG AACTATGGTG CCATCCCTCA GACTTGGGAA GACCCAGGGC ACAATGATAA 420
ACATACTGGC TGTGTGGTG ACAATGACCC AATTGATGTG TGTGAAATTG GAAGCAAGGT 480
ATGTGCAAGA GGTGAAATAA TTGGCGTGAA AGTTCTAGGC ATATTGGCTA TGATTGACGA 540
AGGGGAAACC GACTGGAAAG TCATTGCCAT TAATGTGGAT GATCCTGATG CAGCCAATTA 600
TAATGATATC AATGATGTCA AACGGCTGAA ACCTGGCTAC TTAGAAGCTA CTGTGGACTG 660
GTTTAGAAGG TATAAGGTTT CTGATGGAAA ACCAGAAAAT GAGTTTGCGT TTAATGCAGA 720
ATTTAAAGAT AAGGACTTTG CCATTGATAT TATTAAAAGC ACTCATGACC ATTGGAAAGC 780
ATTAGTGAAT AAGAAAACGA ATGGAAGAGG AATCAGTTGC ATGAATACAA CTTTGTCTGA 840
GAGCCCCTTC AAGTGTGATC CTGATGCTGC CAGAGCCATT GTGGATGCTT TACCACCACC 900
CTGTGAATCT GCCTGCACAG TACCAACAGA CGTGGATAAG TGGTTCCATC ACCAGAAAAA 960
CTAATGAGAT TTCTCTGGAA TACAAGCTGA TATTGCTACA TCGTGTTCAT CTGGATGTAT 1020
TAGAAGTAAA AGTAGTAGCT TTCAAAGCT TTAAATTTGT AGAACTCATC TAACTAAAGT 1080
AAATTCTGCT GTGACTAATC CAATATACTC AGAATGTTAT CCATCTAAAG CATTTTTCAT 1140
ATCTCAACTA AGATAACTTT TAGCACATGC TTAAATATCA AAGCAGTTGT CATTTGGAAG 1200
TCACTTGTGA ATAGATGTGC AAGGGGAGCA CATATTGGAT GTATATGTTA CCATATGTTA 1260
GGAAATAAAA TTATTTTGCT GAACTTGGA AAAAAAAA AAA 1303

```

(2) INFORMATION ON SEQ ID NO. 273:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1586 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

CGGCTCGAGC GGCTCGAGAT TCGAGGTCGT GGTGGTCTTG GAAGAGCGTC GAGGGGGCCG 60
TGGACGTGGA ATGGGCCGAG GAGATGGATT TGATTCTCGT GGCAAACGTG AATTGATAG 120
GCATAGTGGA AGTGATAGAT CTGGCCTGAA GCACGAGGAC AAACGTGGAG GTAGCGGATC 180
TCACAACCTGG GGAACGTGCA AAGACGAATT AACAGAGTCC CCCAAATACA TTCAGAAACA 240
AATATCTTAT AATTACAGTG ACTTGGATCA ATCAAATGTG ACTGAGGAAA CACCTGAAGG 300
TGAAGAACAT CATCCAGTGG CAGACACTGA AAATAAGGAG AATGAAGTTG AAGAGGTAAA 360

```

```

AGAGGAGGGT CCAAAAGAGA TGACTTTGGA TGAGTGGAAG GCTATTCAAA ATAAGGACCG 420
GGCAAAAGTA GAATTTAATA TCCGAAAACC AAATGAAGGT GCTGATGGGC AGTGGAAAGAA 480
GGGATTTGTT CTTCAATAAT CAAAGAGTGA AGAGGCTCAT GCTGAAGATT CGGTTATGGA 540
CCATCATTTT CGGAAGCCAG CAAATGATAT AACGTCTCAG CTGGAGATCA ATTTTGGAGA 600
CCTTGGCCGC CCAGGACGTG GCGGCAGGGG AGGACGAGGT GGACGTGGGC GTGGTGGGCG 660
CCCAAACCGT GGCAGCAGGA CCGACAAGTC AAGTGCTTCT GCTCCTGATG TGGATGACCC 720
AGAGGCATTC CCAGCTCTGG CTTAAGTGA TGCCATAAGA CAACCCTGGT TCCTTTGTGA 780
ACCCTTCTGT TCAAAGCTTT TGCATGCTTA AGGATTCCAA ACGACTAAGA AATTAATAAA 840
AAAAAGACTG TCATTCATAC CATTACACAC TAAAGACTGA ATTTTATCTG TTTTAAAAAT 900
GAACTTCTCC CGCTACACAG AAGTAACAAA TATGGTAGTC AGTTTGTAT TTAGAAATGT 960
ATTGGTAGCA GGGATGTTT CATAATTTT AGAGATTATG CATTCTTCAT GAATACTTTT 1020
GTATTGCTGC TTGCAAATAT GCATTTCCAA ACTTGAAATA TAGGTGTGAA CAGTGTGTAC 1080
CAGTTTAAAG CTTTCACTTC ATTTGTGTTT TTTAATTAAG GATTTAGAAG TTCCCCCAAT 1140
TACAAACTGG TTTTAAATAT TGGACATACT GGTTTTAATA CCTGCTTTGC ATATTCACAC 1200
ATGGTCAACT GGGACATGTT AAACCTTTGAT TTGTCAAATT TTATGCTGTG TGGAAATACT 1260
ACTATATGTA TTTTAACTTA GTTTTAATAT TTTCATTTT GGGGAAAAAT CTTTTTTCAC 1320
TTCTCATGAT AGCTGTTATA TATATATGCT AAATCTTTAT ATACAGAAAT ATCAGTACTT 1380
GAACAAATTC AAAGCACATT TGGTTTATTA ACCCGTGGCT GCCCTGGCAT GGGGCCCCATT 1440
TGGGGTCCAA ATTATACTG ATTTACATTT TCAGCGATAT TACTTTTAAA TGCCTGAGTT 1500
CCCATTTAAA ATCTAACTAG ACACCTAATG GGGAAGTGGT TAACCACTAT GTGGTAGCCA 1560
CGGGCCAG

```

(2) INFORMATION ON SEQ ID NO. 274:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 144 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

KQVKCAKVS Y LLFLFQYCAI DSCIKEFNAG SSWLSSVTLW SMSSVSLSAS NVGRVRIKSE 60
GCSTGDKLSL GVPASKATEP ISFRRSSCS LCCWLSALAS DFFRRSYSGR YLSYSSAAL120
VTCTKSSSNP VPRTAETPTT LSEL

```

(2) INFORMATION ON SEQ ID NO. 275:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 143 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Name: 275 Len: 143 Check: 15DA
MSLVLDEFYS SLRVVGVS AV LGTGLDEL FV QVTSAAEEYE REYRPEYERL KKSLANAESQ 60
QREQLERLR KDMGSVALDA GTPKDSLSPV LHPSDLILTR PTLEADSDTD DIDHRVTEES120
HEEPAFQNF M QESMAQYWKR NNK 143

(2) INFORMATION ON SEQ ID NO. 276:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 181 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

IPNMAAPLGG MFSGQPPGPP QAPPGLPGQA SLLQAAPGAP RPSSSTLVDE LESSFEACFA 60
SLVSQDYVNG TDQEEIRTGV DQCIQKFLDI ARQTECFLLQ KRLQLSVQKP EQVIKEDVSE120
LRNELQRKDA LVQKHLTKLR HWQQVLEDIN VQHKKPADIP QGSLAYLEQA SANIPAPLKP180
T 181

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 89 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

NELIIWQRLV PKCQVHRKEC VANLTHQPTH RPTASALCSR WLQRCRDVGR CLLQVGQGAL60
RDVGGFLFVLH VDVLLQHLLPM PQLCQVLLD 89

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 401 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

MPNFCAAPNC TRKSTQSDLA FFRFPRDPA CQKWVENCRR ADLEDKTPDQ LNKHYRLCAK 60
 HFETSMICRT SPYRTVLRDN AIPTIFDLTS HLNPNHSRHR KRIKELSEDE IRTLKQKKID120
 ETSEQEQKHK ETNNSNAQNP SEEEGEGQDE DILPLTLEEK ENKEYLKSLE EILILMGKQN180
 IPLDGHEADE IPEGLFTPDN FQALLECRIN SGEEVLRKRF ETTAVNTLFC SKTQQRQMLE240
 ICESCIREET LREVRDSHFF SIITDDVVDI AGEHLPVLV RFVDESHNL R EEFIGFLPYE300
 ADAEILAVKE HTMITKWL NMEYCRGQAY IVSSGFSSKM KVVASRLLEK YPQAIYTLCS360
 SCALNMWLAK SVPVMGVSVA LGTIEEVCSF FHXITTTAFR T 401

(2) INFORMATION ON SEQ ID NO. 279:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 106 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

MLISGTL SHG TTQIQYXXEE HHADMYRSDL PNPDTLSAEL HCWRIKWKHR GKDIPLPSTI 60
 YEALHLPDIK FFPNVYALLK VLCILPVMKV ENERYENGTK ASLKHI 106

(2) INFORMATION ON SEQ ID NO. 280:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 398 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
GRKCNKFWDN AQTSGIEEPS ETKGSMQKSK FKYKLVPEEE TTASENTEIT SERQKEGIKL 60
TIRISSRKKK PDSPPKVLEP ENKQEKTEKE EEKTNVGRTL RRSRPRISPT AKVAEIRDQK120
ADKKRGEDED EEEEEESTALQ KTDKKEILKK SEKDTNSKVS KVKPKGKVRW TGSRTGRWK180
YSSNDESEGS GSEKSSAASE EEEEEKESEE ILADDDPECK KCGLPNHPEL ILLCDSCDSG240
YHTACLRPPL MIIPDGEWFC PPCQHKLLCE KLEEQLQDLD VALKKKERAE RRKERLVYVG300
ISIEINIIPPQ EPDFSEDQEE KKKDSKKS KA NLLERRSTRT RKCISYRFDE FDEAIDEAIE360
DDIKEADGGG VGRGKDISTI TGHGKDIST ILDEKIIT 398
```

(2) INFORMATION ON SEQ ID NO. 281:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 198 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```
SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSSNFSQS SLCWQGGQNH 60
SPSGMIIRGG RRQAVWYPLS QESHRRISG WFGPHFLHG SSSSARMAS LSFSSSSEAI120
ADDFSLPDPS LSSLLEYFHL PRVREPVHRT LPLGFTLLTL EFVSFSDFFK ISFLSVFCKA180
VDSSSTSSSP SPLFLSAF 198
```

(2) INFORMATION ON SEQ ID NO. 282:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 202 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

GRLPFSGRGR GKKVTSGDGV ASLPLKLGRL FGGVTRGFNM RIEKCYFCSG PIYPGHGMMF 60
 VRNDCKVFRF CKSKCHKNEK KKRNPVKVRW TKAFRKAAGK ELTVDNSFEF EKRRNEPIKY120
 QRELWNKTID AMKRVEEIKQ KRQAKFIMNR LKKNKELQKV QDIKEVKQNI HLIRAPLAGK180
 GKQLEEKMVQ QLQEDVDMED AP 202

(2) INFORMATION ON SEQ ID NO. 283:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 84 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF**(iii) HYPOTHETICAL: yes****(vi) ORIGIN****(A) ORGANISM: HUMAN****(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:**

ITHCKLFTSC FPECFGPPNF ARIALLFKVF MTRFAKSEH LAIVADEHHA VSRIDGPRTE60
 ITLFDTHVEP ACNPTKQTPK LERK 84

(2) INFORMATION ON SEQ ID NO. 284:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 206 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF**(iii) HYPOTHETICAL: yes****(vi) ORIGIN****(A) ORGANISM: HUMAN****(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:**

RLEPRSVTRS RRAVSRLSAR PGKVSAMAF LASGPYLTHQ QKVLRLYKRA LRHLESWCVQ 60
 RDKYRYFACL MRARFEEHKN EKDMAKATQL LKEAEEEFWY RQHPQPYIFP DSPGGTSYER120
 YDCYKVPWC LDDWHPSEKA MYPDYFAKRE QWKKLRRESW EREVQLQEE TPPGGPLTEA180
 LPPARKEGDL PPLWWYIVTR PRERP 206

(2) INFORMATION ON SEQ ID NO. 285:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 139 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRCAV 60
 DADGTRILPR PPSAAGWPSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVAPAYKAA120
 TPFADGSGRV PTPRTPLRR 139

(2) INFORMATION ON SEQ ID NO. 286:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRELLD SWSGVIPFF FSCSCLPFLY60
 PPRWRQIHDL KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 287:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SWSGVIPFF FSCSCLPFLY60
PPKWROIHDL KDTQYLLNSS 80

(2) INFORMATION ON SEQ ID NO. 288:

(i) SEQUENCE CHARACTERISTIC:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) **HYPOTHETICAL:** yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

RLSCAGTLSG  SGPHPSSRLT  QGRWVRKSRV  AMEKIPVSAF  LLLVALSYTL  ARDTTVKPGA  60
KKDKTDSRPK  LPQTLSRGWG  DQLIWTQTYE  EALYKSKTSN  KPLMIIHHL  ECPHSQALKK 120
VFAENKEIQK  LAEQFVLLNL  VYETTDKHL  PDGQYVPRIM  FVDPSLTVRA  DITGRYSNRL 180
YAYEPADTAL  LLDNMKKALK  LLKTEL
                                                    206

```

(2) INFORMATION ON SEQ ID NO. 289:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 77 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GNPELPWRKE QCQHSCSLWP SPTLWPEIQ SNLEPKRTQR TLDPNCPRPS PEVGVTNSSG60
LRHMKKLYIN PRQATNP 77

(2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGXGXQLLXP XAXQGXAAS CXXQDVHLXR CXTVVRWYQR ITGMPXXAPT RNFSKFQRXV 60
 MDLHGFPKEX GXEXQEXLQ WEGRSSSGKC RISXSXLPXS TIXXFLKXXW XXIRXQSPXT120
 WXRTYLRGSG ISEFSPGSCL PNWLEGKPRM TXAKWPKFFL 160

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

RHXPLXLGXH GHRAHSCLGW SOXALWDXAW GLXXXGSXQX RKKEAXWCVX VGXVGXCXXP 60
 XEXMXXGFQ NXXGPNXXV SXLGXXXWNR XAEKNMXGCC AKXVNXMDH XXGFQXRQIR120
 GLCSHAHTGX NCHVSXSGSD TQLCXGLSFM 150

(2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

RAAKILKGGL QEVAEQLELE RIGPQHQAGS DSSLTGMAFF KMREMFFEDH IDDAKYCGHL60
YGLGSGSSYV QNGTGNAYEE EANKQS 86

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 64 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

IKAKFNLNAF FFFFLLRSEI GTVILSTERQ TIKWAMKGGG KVLIVRGIQ PEIKPIYKHV60
CSSK 64

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 226 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ASTIMDLLFG RRKTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIID IKKMAKQGQM 60
DAVRIMAKDL VRTRRYVRKF VLMRANIQAV SLKIOTLKSN NSMAQAMKGV TKAMGTMNRQ120
LKLPIQKIM MEFERQAEIM DMKEEMMND A IDDPMGDEED EEESDAVVSQ VLDELGLSLT180
DELSNLPSTG GSLSVAAGGK KAEAAASALA DADADLEERL KNLRRD 226

(2) INFORMATION ON SEQ ID NO. 295:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 166 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

KILGIHWLSR SGRGTQSLRR FLSRSSRSAS ASARAEAAAS AFFPPAATLS EPPVEGRFDS 60
 SSVRLSPSSS RTWDTTASLS SSSSSSPMGS SMASFISSF ISMISACRSN SIMIFWIWGN120
 FSCLEFVPMALVTPFMACAI ELLDLSVWIL RDTAWMLARI NTNLR 166

(2) INFORMATION ON SEQ ID NO. 296:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 233 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

KPEGARRVQF VMGLFGKTQE KPPKELVNEW SLKIRKEMRV VDRQIRDIQR EEEKVKRSVK 60
 DAAKKGQKDV CIVLAKEMIR SRKAVSKLYA SKAHMNSVLM GMKNQLAVLR VAGSLQKSTEL20
 VMKAMQSLVK IPEIQATMRE LSKEMMKAGI IEEMLEDTFE SMDDQEEMEE EAEMEIDRIL180
 FEITAGALGK APSKVTDALP EPEPPGAMAA SEDEGEEEEE LEAMQSRLAT LRS 233

(2) INFORMATION ON SEQ ID NO. 297:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 129 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

LMPFQSQNLQ ERWLPQRMRG RRRKRLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60
 ALHLCCEDYH FEGGSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRSIDRY ILLWGGERNP120
 SAHEALLKI 129

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 351 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TWCTTTMLAA RLVLRLTPS RVFHPAFTKA SPVVKNSITK NQWLLTPSRE YATKTRIGIR 60
 RGRGTGQELKE AALEPSMEKI FKIDQMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIEKAV120
 IWPQYVKDRI HSTYMYLAGS IGLTALSAIA ISRTPVLMNF MMRGSWVTIG VTFAAMVGAG180
 MLVRSIPYDQ SPGPKHLAWL LHSGVMGAVV APLTILGGPL LIRAAWYTAG IVGGLSTVAM240
 CAPSEKFLNM GAPLGVGLGL VEVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFSMFLLYD300
 TQKVIKRAEV SPMYGVQKYD PINSMLSIYM DTLNIFMRVA TMLATGGNRK K 351

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RVAPATVVGG RNIDPNEDTK TRPRPTPRGA PMERNFSLGA HMATVERPPT MPAVYHAALM 60
 RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120
 MKFMRTGVLL IAMADKAVKP ILPAKYI 147

(2) INFORMATION ON SEQ ID NO. 300:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 188 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

RRLEVSRYQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEYQSL 60
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLLKYE FDIEFDIPIT YPTTAPEIAV120
 PELDGKTAKM YRGGKICLTD HFKPLWARNV PKFGLAHLMA LGLGPWLAVE IPDLIQKGV180
 QHKEKCNQ 188

(2) INFORMATION ON SEQ ID NO. 301:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 172 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

SKFGHIPGPQ RFEMIRQAYF ATPVHLCCLS IQLRNCNFWG SSRICDRNVK LDVKLIFQEV 60
 MDIPAFSKPP SSFLVGLQSE PIVVSILVVL HIPDKGLIFL LQSLHPQLTI SGSGVSLQHR120
 DLRHNTSRGF IRHLGPGRKR NAEVVLPVAY LKAPSSLLWE DETLGCKTS FE 172

(2) INFORMATION ON SEQ ID NO. 302:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 320 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60
 SPFHDIPIYA DKDVFMVVE VPRWSNAKME IATKDPLNPI KQDVKKGKLR YVANLFPYKG120
 YIWNYGAIPQ TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180
 GETDWKVIAl NVDDPDAANY NDINDVKRLK PGYLEATVDW FRRYKVPD GK PENEFAFNAE240
 FKDKDFAIDI IKSTHDHWKA LVTKKTNGKG ISCMNTTlse SPFKCDPDAA RAIVDALPPP300
 CESACTVPTD VDKWFHHQKN 320

(2) INFORMATION ON SEQ ID NO. 303:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

RVLCSNLHFC IRPAWYFNYH VKHILICINW NIMKWRYILS FLIFEEDSVL QGEGRGALLG60
 AEAHSAGVL PPPLPQSHQP ARGAD 85

(2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 247 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGGSGS 60
 HNWTGTVKDEL TESPKEYIQKQ ISYNYSDLDQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120
 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSSE EAAHEDSVMD180
 HHFRKPANDI TSQLEINFGD LGRPGRGGRG GRGGRGRGGR PNRGSRTDKS SASAPDVDDP240
 EAFPALA

247

(2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

SFGILKHAKA LNRRVHKGTR VVLWHPVKPE LGMPLGHPHQ EQKHLTCRSC CHGLGAHHAH60
 VHLVLPCHRV LGGQGLQN

78

(2) INFORMATION ON SEQ ID NO. 306:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 293 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ATRGAEQDGG ASAARPRRRW AGGLLQRAAP CSLLPRLRTW TSSSNRSRED SWLKSLEVRK 60
 VDFPRKDAHSN LLAKKETSNI YKLQFHNVPK ECLEAYNKIC QEVLPKIHED KHYPCITLVGT120
 WNTWYGEQDQ AVHLWRYEGG YPALTEVMNK LRENKEFLEF RKARSDMLLS RKNQLLLEFS180
 FWNEPVPRSG PNIYELRSYQ LRPGMTIEWG NYWARAIRFR QDGNEAVGGF FSQIGQLYMV240
 HHLWAYRDLQ TREDIRNAAW HKHGWEELVY YTVPLIQEME SRIMIPLKTS PLQ 293

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 208 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

AHRNSTALLE GRGLQWDHDS GFHFLNKWNC VIYQFLPAMF VPCCIPYVFP GLKIPVSPKM 60
 VHHVQLPNLR EESSDGFVTI LSEADCTSPV IAPFNHGSWS ELVRPEFIYI RSGSWHRLIP120
 ETELQOELIL PGEKHVTSC LTKFQKFLIFS EFIHDFCEGW IASFIPPEVD SLVLLAIPRV180
 PSPHQSTRVV FIFVNLWQHL LTNEFVVCF 208